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OM nucleic - nucleic search, using sw model

Run on: April 27, 2005, 17:25:16 ; Search time 1427 Seconds
(without alignments)
10835.997 Million cell updates/sec

Title: US-09-989-739-18
Perfect score: 2547
Sequence: 1 ccattggtcgatccttcccc.....gctggtggtgctgtcgtt 2547

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5633728 seqs, 303525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2547	100.0	2547	10	US-09-989-739-18
2	399	15.7	2291	18	US-10-425-115-86750
3	203	8.0	957	17	US-10-425-114-1414
c	181	7.1	289	18	US-10-425-115-32558
5	132	5.2	1044	18	US-10-425-115-141079
6	132	5.2	1316	17	US-10-425-114-22834
7	132	5.2	1342	18	US-10-425-115-141080
8	132	5.2	1359	17	US-10-425-114-19533
9	132	5.2	1413	17	US-10-425-114-17319
10	132	5.2	1426	17	US-10-425-114-773
11	132	5.2	1605	17	US-10-425-114-32327

12	132	5.2	1638	18	US-10-425-115-141081	Sequence 141081,
13	132	5.2	1800	18	US-10-425-115-141084	Sequence 141084,
14	122.4	4.8	706	18	US-10-767-701-12658	Sequence 12658, A
15	108	4.2	860	18	US-10-425-115-165740	Sequence 165740,
16	107.2	4.2	3001	16	US-10-338-777-4	Sequence 4, Appli
17	104.8	4.1	1093	17	US-10-425-114-36130	Sequence 36130, A
18	104.8	4.1	1353	17	US-10-425-114-30712	Sequence 30712, A
19	104.8	4.1	1431	17	US-10-425-114-35310	Sequence 35310, A
20	104.8	4.1	1440	17	US-10-425-114-1405	Sequence 1405, Ap
21	104.8	4.1	1463	17	US-10-425-114-22195	Sequence 22195, A
22	104.8	4.1	1622	18	US-10-425-115-10088	Sequence 10088, A
23	104.8	4.1	1623	18	US-10-425-115-67912	Sequence 67912, A
24	104	4.1	1524	18	US-10-739-930-2495	Sequence 2495, Ap
25	103.2	4.1	1326	17	US-10-425-114-14399	Sequence 14399, A
26	103.2	4.1	1376	18	US-10-425-115-110179	Sequence 110179,
27	103.2	4.1	1431	18	US-10-425-115-109303	Sequence 109303,
28	103.2	4.1	1456	17	US-10-425-114-27579	Sequence 27579, A
29	103.2	4.1	1490	18	US-10-739-930-2497	Sequence 2497, Ap
30	103.2	4.1	1503	17	US-10-425-114-22084	Sequence 22084, A
31	103.2	4.1	1508	17	US-10-425-114-21570	Sequence 21570, A
32	103.2	4.1	1561	18	US-10-425-115-67911	Sequence 67911, A
33	103.2	4.1	1568	18	US-10-437-963-28028	Sequence 28028, A
34	103.2	4.1	1570	18	US-10-425-115-109304	Sequence 109304,
35	103.2	4.1	2078	18	US-10-425-115-108405	Sequence 108405,
36	102.2	4.0	1392	17	US-10-425-114-21120	Sequence 21120, A
37	102.2	4.0	2438	18	US-10-425-115-67915	Sequence 67915, A
38	101.4	4.0	1348	17	US-10-425-114-30956	Sequence 30956, A
39	101.4	4.0	1348	18	US-10-425-115-67904	Sequence 67904, A
40	101	4.0	281	9	US-09-923-876-4439	Sequence 4439, Ap
41	101	4.0	281	10	US-09-923-876-4439	Sequence 4439, Ap
42	100.6	3.9	1352	17	US-10-425-114-21011	Sequence 21011, A
43	100.6	3.9	1552	18	US-10-425-115-10090	Sequence 10090, A
44	98.6	3.9	693	17	US-10-260-238-5656	Sequence 5656, Ap
c	45	98.4	1915	18	US-10-767-701-15746	Sequence 15746, A

ALIGNMENTS

= instant cage

RESULT 1
US-09-989-739-18
; Sequence 18, Application US/09989739
; Publication No. US20030140364A1
; GENERAL INFORMATION:
; APPLICANT: HINCHEY, BRENDAN
; APPLICANT: SONG, HEE-SOOK
; TITLE OF INVENTION: MAIZE CYTOPLASMIC GLUTAMINE SYNTHETASE PROMOTER
; FILE REFERENCE: DEKM:177US
; CURRENT APPLICATION NUMBER: US/09/989,739
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 2547
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-989-739-18

Query Match	100.0%	Score 2547;	DB 10;	Length 2547;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2547;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CCATGGTCCGTACCTTCCCTCGCTGCACGAAATGAACCGACCTGTTGCGTACAGACATT	60	
Db	1	CCATGGTCCGTACCTTCCCTCGCTGCACGAAATGAACCGACCTGTTGCGTACAGACATT	60	
QY	61	TCGTGGAATGGTCTTCTTACGCTGAGCCTGTGTAATCCAGGTTCCGGATTGAGCAGG	120	
Db	61	TCGTGGAATGGTCTTCTTACGCTGAGCCTGTGTAATCCAGGTTCCGGATTGAGCAGG	120	

Db 2281 AATATATTAATATAGATAGATATATTTCTCACCACAAATCACTACAGTACAAATTCACG 2340
Qy 2341 AGTGACCGCGATGAGTCGAGAGACAAACGTTACCGCGCCCTTGCGAGAACACTTTCC 2400
Db 2341 AGTGACCGCGATGAGTCGAGAGAACCGTTACCGCGCCCTTGCGAGAACACTTTCC 2400
Qy 2401 AAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTGCTCTATTTATGAGGAGCAGCC 2460
Db 2401 AAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTGCTCTATTTATGAGGAGCAGCC 2460
Qy 2461 AGCTACAGGCTACAGCGTGGGAAAGACACACGAGTCAATCACTCATCTCGGGGCA 2520
Db 2461 AGCTACAGGCTACAGCGTGGGAAAGACACACGAGTCAATCACTCATCTCGGGGCA 2520
Qy 2521 TTGTCTCTGCTCGTGGCTCTCTGCTT 2547
Db 2521 TTGTCTCTGCTCGTGGCTCTCTGCTT 2547
RESULT 2
US-10-425-115-86750
; Sequence 86750, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 86750
; LENGTH: 2291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_179122C.1
US-10-425-115-86750
Query Match 15.7%; Score 399; DB 18; Length 2291;
Best Local Similarity 100.0%; Pred. No. 2e-73;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATGGTCCGTACCTTCCCTGCGACGAAATGAACCGACCTGTTCGTACAGACATT 60
Db 526 CCATGGTCCGTACCTTCCCTGCGACGAAATGAACCGACCTGTTCGTACAGACATT 585
Qy 61 TCGTCGAAATGGTTCTTACGCTGAGCCTGTGTAATCCAGTTTCGGGATTGAGCAGG 120
Db 586 TCGTCGAAATGGTTCTTACGCTGAGCCTGTGTAATCCAGTTTCGGGATTGAGCAGG 645
Qy 121 AGTACACCTTCTCCAGAGGACACCAAGTGGCTCTCGGTTGGCGCTGGCGGCTACC 180
Db 646 AGTACACCTTCTCCAGAGGACACCAAGTGGCTCTCGGTTGGCGCTGGCGGCTACC 705
Qy 181 CTGGCCCTCAGGTAGATTAGATTCGATTCGCTCCAGGCTCCAGCCATATCGATGGC 240
Db 706 CTGGCCCTCAGGTAGATTAGATTCGATTCGCTCCAGGCTCCAGCCATATCGATGGC 765
Qy 241 TTTGATCAGCTGACGGATATCTTGGCAGGACCTTACTACTGCGCTCGGAGCGGAC 300
Db 766 TTTGATCAGCTGACGGATATCTTGGCAGGACCTTACTACTGCGCTCGGAGCGGAC 825
Qy 301 AAGTCTTACGGCGGACATCGTGACGCGCACTACAGGCTGCTCTACGCGGCAATC 360
Db 826 AAGTCTTACGGCGGACATCGTGACGCGCACTACAGGCTGCTCTACGCGGCAATC 885
Qy 361 GACATCAGTGCATCAACGGGAGGTATCGCGGGCAG 399

Db 886 GACATCAGTGCATCAACGGGAGGTATCGTCCGGGCGCAG 924
RESULT 3
US-10-425-114-1414
; Sequence 1414, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 1414
; LENGTH: 957
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700152411_FLI
US-10-425-114-1414
Query Match 8.0%; Score 203; DB 17; Length 957;
Best Local Similarity 78.7%; Pred. No. 2.2e-32;
Matches 292; Conservative 0; Mismatches 0; Indels 79; Gaps 1;
Qy 29 CGAAATGAACCGACCTGTTCGTACAGACATTTCTCGAAATGGTTCTTTACGCTGAG 88
Db 1 CGAAATGAACCGACCTGTTCGTACAGACATTTCTCGAAATGGTTCTTTACGCTGAG 60
Qy 89 CCTGTGTAATCCAGTTTCGGGATTGAGCAGGAGTACACCTTCTCCAGAGGACACCAA 148
Db 61 CCTGTGTAATCCAGTTTCGGGATTGAGCAGGAGTACACCTTCTCCAGAGGACACCAA 120
Qy 149 GTGGCCTCTCGTTGGCGCTGGCGGCTACCTTGGCGCTCAGGTAGATTAGATGGATCT 208
Db 121 GTGGCCTCTCGTTGGCGCTGGCGGCTACCTTGGCGCTCAGGTAGATTAGATGGATCT 160
Qy 209 GCGTGCCTCCAGGCTCCAGCCATATCGATGCTTTGATCAGCTGACGGAATGATCCTGGC 268
Db 161 -----C 161
Qy 269 AGGACCTTACTACTGCGCGCTCGGAGCGGACAAAGTCTTACGGCGGACATCGTGGACG 328
Db 162 AGGACCTTACTACTGCGCGCTCGGAGCGGACAAAGTCTTACGGCGGACATCGTGGACG 221
Qy 329 CGCATCAGAGGCTGCTCTTACCGCGCATCGACATCAGTGGCATCAACGGGAGGTCA 388
Db 222 CGCATCAGAGGCTGCTCTTACCGCGCATCGACATCAGTGGCATCAACGGGAGGTCA 281
Qy 389 TGCCGGGCGCAG 399
Db 282 TGCCGGGCGCAG 292
RESULT 4
US-10-425-115-32558/c
; Sequence 32558, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B

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; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 32558
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_129
US-10-425-115-32558

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Query Match          7.1%; Score 181; DB 18; Length 289;
Best Local Similarity 85.8%; Pred. No. 5.3e-28;
Matches 248; Conservative 0; Mismatches 35; Indels 6; Gaps 4;

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Qy	241	TTTGATCAGCTGACGGAAATGATCTCGCAGGACCTTACTACTCGCGCGTCGGA--GCGG	298
Db	289	TTTGATCAGCTGACGCAATGATAGTCGACGGGACCTTCATCTCGCGCGTCGGACCGCA	230
Qy	299	ACAAAGTCCTACGGCGGGACATCGTGACGGCGCACTACAAGGCGTGCCTCTACGCCCGGCA	358
Db	229	CAAGCTCTACGGCGGGGCACATCGTGACGGCGCACTACAGGCGCTGCTATACGCCGGCA	170
Qy	359	TCGACATCA--GTGGCATCAACGGGGAGGTGATGCGGGGAGGTACAGCGTGTGCTCTA	417
Db	169	TCGACATCACAATGGCATCATCGGTGAGGTGATACCGGGGAGGTACAGCGTGTGCTCTA	110
Qy	418	GCTACCTTGTCTTTAACTGGACACCTGCACCTCTGCACACTGCACAGCTAGT--AGTATGCTG	476
Db	109	GCTCCCTTGTCTTCCCTTGCACACCGGCATTTTGCACACTGCTCAGCTAGTCAGTATGCTG	50
Qy	477	CTATCTCTGTCGACCCCA--GGCTTTGTCGTGGACAGTGGGAGTTCCAGG	523
Db	49	CCATCTCTGTCTCACTACAGGCTTGTTCAGGGTTTCAGTCGGAGTTCGAGG	1

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RESULT 5
US-10-425-115-141079
; Sequence 141079, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 141079
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_60146C.1
US-10-425-115-141079

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Query Match      5.2%; Score 132; DB 18; Length 1044;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	268	CAGGGA	CCTTACT	TACTG	CGCGGT	CGGAG	CGGACA	AGTCT	TACGG	CGGGAC	ATCGT	GGAC	327	
Db	307	CAGGGA	CCTTACT	TACTG	CGCGGT	CGGAG	CGGACA	AGTCT	TACGG	CGGGAC	ATCGT	GGAC	366	
Qy	328	GGC	CAC	TAC	AAG	GCT	GCCTT	ACG	CGGGAT	CGACAT	CAGT	GGCAT	CAACGGGAGGTC	387
Db	367	GGC	CAC	TAC	AAG	GCT	GCCTT	ACG	CGGGAT	CGACAT	CAGT	GGCAT	CAACGGGAGGTC	426
Qy	388	ATC	CGGGG	CAG	399									

Db 427 ATGCCGGGCAG 438

RESULT 6

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US-10-425-114-22834
; Sequence 22834, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22834
; LENGTH: 1316
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3591-121-H10_FLI
US-10-425-114-22834

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Query Match	5.2%	Score 132;	DB 17;	Length 1316;
Best Local Similarity	100.0%;	Pred. No. 2.3e-17;		
Matches 132; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	268	CAGGGACCTTACTACTACTGCGCGGTGAGCGGACAAGTCTTACGGCGGGACATCGTGAC	327
Db	514	CAGGGACCTTACTACTGCGCGGTGAGCGGACAAGTCTTACGGCGGGACATCGTGAC	573
Qy	328	GCGCACTACAAGGCGCTGCTCTACGCGGCAATCGACATCAGTGGCATCAACGGGAGGTC	387
Db	574	GCGCACTACAAGGCGCTGCTCTACGCGGCAATCGACATCAGTGGCATCAACGGGAGGTC	633
Qy	388	ATCGCGGGGCGAG	399
Db	634	ATCGCGGGGCGAG	645

RESULT 7

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US-10-425-115-141080
; Sequence 141080, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 141080
; LENGTH: 1342
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_60147C.1
US-10-425-115-141080

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Query Match 5.2%; Score 132; DB 18; Length 1342;
 Best Local Similarity 100.0%; Pred. No. 2.3e-17;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 CAGGGACCTTACTACTCGCGTGGAGCGGACAAAGTCTTACGGGGCGGACATCGTGAC 327

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Db      514 CAGGACCTTACTACTGCGCGTCTACGCGGACAAAGTCTCTACGGCGGGACATCGTGGAC 573
Qy      328 GCGCACTACAAGCCTGCTCTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db      574 GCGCACTACAGGCTGCTCTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 633
Qy      388 ATGCCGGGGCAG 399
Db      634 ATGCCGGGGCAG 645

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RESULT 8
US-10-425-114-19533
; Sequence 19533, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19533
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-045-F7_FLI
US-10-425-114-19533

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Query Match      5.2%; Score 132; DB 17; Length 1359;
Best Local Similarity 100.0%; Pred. No. 2.3e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      268 CAGGACCTTACTACTGCGCGTCTACGCGGACAAAGTCTCTACGGCGGGACATCGTGGAC 327
Db      563 CAGGACCTTACTACTGCGCGTCTACGCGGACAAAGTCTCTACGGCGGGACATCGTGGAC 622
Qy      328 GCGCACTACAAGCCTGCTCTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db      623 GCGCACTACAAGCCTGCTCTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 682
Qy      388 ATGCCGGGGCAG 399
Db      683 ATGCCGGGGCAG 694

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RESULT 9
US-10-425-114-17319
; Sequence 17319, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 17319
; LENGTH: 1413

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; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3069-006-G11_FLI
US-10-425-114-17319

Query Match      5.2%; Score 132; DB 17; Length 1413;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      268 CAGGACCTTACTACTGCGCGTCTACGCGGACAAAGTCTCTACGGCGGGACATCGTGGAC 327
Db      454 CAGGACCTTACTACTGCGCGTCTACGCGGACAAAGTCTCTACGGCGGGACATCGTGGAC 513
Qy      328 GCGCACTACAAGCCTGCTCTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db      514 GCGCACTACAAGCCTGCTCTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 573
Qy      388 ATGCCGGGGCAG 399
Db      574 ATGCCGGGGCAG 585

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RESULT 10
US-10-425-114-773
; Sequence 773, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 773
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700092738_FLI
US-10-425-114-773

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Query Match      5.2%; Score 132; DB 17; Length 1426;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      268 CAGGACCTTACTACTGCGCGTCTACGCGGACAAAGTCTCTACGGCGGGACATCGTGGAC 327
Db      541 CAGGACCTTACTACTGCGCGTCTACGCGGACAAAGTCTCTACGGCGGGACATCGTGGAC 600
Qy      328 GCGCACTACAAGCCTGCTCTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db      601 GCGCACTACAAGCCTGCTCTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 660
Qy      388 ATGCCGGGGCAG 399
Db      661 ATGCCGGGGCAG 672

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RESULT 11
US-10-425-114-32327
; Sequence 32327, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

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CC potato, soybean, cotton, canola, alfalfa, sunflower, and cotton).
 CC Preferably, the monocotyledonous or dicotyledonous plant is maize or
 CC soybean plant, respectively. The promoter is useful for directing the
 CC expression of a selected coding region which encodes a particular protein
 CC or polypeptide product, improving feed or food value, improving
 CC processing of corn and for improving the value of the product resulting
 CC from the processing. The promoter is efficient in expressing transgenes
 CC in plants. The present sequence represents maize GSI-2 promoter.
 XX

SQ Sequence 2547 BP; 691 A; 602 C; 574 G; 680 T; 0 U; 0 Other;

Query Match 100.0%; Score 2547; DB 12; Length 2547;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCATGGTCCGACCTTCCCTCCCTGCAACGAAATGAACGACCTGTTGCGTACAGACATT	60
Db	1	CCATGGTCCGACCTTCCCTCCCTGCAACGAAATGAACGACCTGTTGCGTACAGACATT	60
Qy	61	TCGTGAAATGGTCTTCTTACGCTGAGCCTGTGTAAATCCAGGTTGCGGATTCAGCAGG	120
Db	61	TCGTGAAATGGTCTTCTTACGCTGAGCCTGTGTAAATCCAGGTTGCGGATTCAGCAGG	120
Qy	121	AGTACACCTTCTCCAGAAAGACACCAAGTGGCTCTCGGTTGGCCGTCGGCGGCTACC	180
Db	121	AGTACACCTTCTCCAGAAAGACACCAAGTGGCTCTCGGTTGGCCGTCGGCGGCTACC	180
Qy	181	CTGGCCCTCAGTAGATTAGATCTGCTGCTCCAGGCTCCAGCCATATCGATGGC	240
Db	181	CTGGCCCTCAGTAGATTAGATCTGCTGCTCCAGGCTCCAGCCATATCGATGGC	240
Qy	241	TTTGATCAGCTGACGGAATGATCTGGCAGGACCTTACTACTGCGCGCTCGGAGCGGAC	300
Db	241	TTTGATCAGCTGACGGAATGATCTGGCAGGACCTTACTACTGCGCGCTCGGAGCGGAC	300
Qy	301	AAGTCTTACGGCGGGACATCTGGAGCGCACTACAAAGGCTCCCTCTACGCGCGGATC	360
Db	301	AAGTCTTACGGCGGGACATCTGGAGCGCACTACAAAGGCTCCCTCTACGCGCGGATC	360
Qy	361	GACATCAGTGGCATCAACGGGAGGTCTATGCGGGGAGGTACAGCGTGTCTAGCT	420
Db	361	GACATCAGTGGCATCAACGGGAGGTCTATGCGGGGAGGTACAGCGTGTCTAGCT	420
Qy	421	ACCTTGCTTTAACTGCACTGCACTCTGCACACTGCACTGCACTGCACTGCTAT	480
Db	421	ACCTTGCTTTAACTGCACTGCACTCTGCACACTGCACTGCACTGCACTGCTAT	480
Qy	481	CTCTGCTGACCGAGCTTGTTCGTGGACAGTGGAGTTCCAGGTCGGCCCTGCCGTCGGC	540
Db	481	CTCTGCTGACCGAGCTTGTTCGTGGACAGTGGAGTTCCAGGTCGGCCCTGCCGTCGGC	540
Qy	541	GTCTGCGCGCGGACAGCTGGGTGGCTCGCTACATTTCTTGGAGAAACGGTAGACCTG	600
Db	541	GTCTGCGCGCGGACAGCTGGGTGGCTCGCTACATTTCTTGGAGAAACGGTAGACCTG	600
Qy	601	CCCCCTGCGCGCTGTTGCTTCTTCCGCGAGACATGGCGTGTGGCACTTT	660
Db	601	CCCCCTGCGCGCTGTTGCTTCTTCCGCGAGACATGGCGTGTGGCACTTT	660
Qy	661	GCGGTGTCAGTGTGTTTGTGATGAGACGTGCTCTTCCCTGTCGCTGGCAGAGGATAC	720
Db	661	GCGGTGTCAGTGTGTTTGTGATGAGACGTGCTCTTCCCTGTCGCTGGCAGAGGATAC	720
Qy	721	CGAGATCCGCGCGGTGTTGTTCTTTCGACCCCAACCAATTCGGTAGCATTTCGCTACC	780
Db	721	CGAGATCCGCGCGGTGTTGTTCTTTCGACCCCAACCAATTCGGTAGCATTTCGCTACC	780
Qy	781	AAACATTTTGGGTTTGTATATGTTGGTCTCTGTATCTGTGGTCTCATGTCTGTTGGAT	840
Db	781	AAACATTTTGGGTTTGTATATGTTGGTCTCTGTATCTGTGGTCTCATGTCTGTTGGAT	840
Qy	841	CTGTGCATGCTGACCTGAGTGGCTGTGTCGGCGGTCTCTTCTGTTGTTGGTGGAGTT	900
Db			

Db	841	CTGTGCATGCTGTGACTGCGCTGTGTCGGCGGTCTTCTTCTGTGTGGTTCGGAGTT	900
Qy	901	CGTTCTCTCGTGCACACACACACACACCGGCGAGCCAAACAGTGTAGCTTCGCCCGGTG	960
Db	901	CGTTCTCTCGTGCACACACACACACACCGGCGAGCCAAACAGTGTAGCTTCGCCCGGTG	960
Qy	961	GAATCCGGCAAGTGTCCAAAGGCAAGCTTCAACGGATGCCGATGCTTCGCGCGGCGGG	1020
Db	961	GAATCCGGCAAGTGTCCAAAGGCAAGCTTCAACGGATGCCGATGCTTCGCGCGGCGGG	1020
Qy	1021	AGAGCTTGGCGGAGCGACTCGTCATCGGATCGGATACGACGCGTTGGATCGGAGATCG	1080
Db	1021	AGAGCTTGGCGGAGCGACTCGTCATCGGATCGGATACGACGCGTTGGATCGGAGATCG	1080
Qy	1081	GAGCGCTTTTGAATTTGCCCTGTCTATCATCTGTACCTGTACCGTGTGCGGTGCTCCA	1140
Db	1081	GAGCGCTTTTGAATTTGCCCTGTCTATCATCTGTACCTGTACCGTGTGCGGTGCTCCA	1140
Qy	1141	TGATATTTATTTGTTGTAATTTGCAAAATTCGTATGTAAATAAATAAATAAATAATG	1200
Db	1141	TGATATTTATTTGTTGTAATTTGCAAAATTCGTATGTAAATAAATAAATAAATAATG	1200
Qy	1201	AAGTAGTATCAGAAATGATCGGACGTCGAAATACCGTAAGAAATGACCGGACGTCGCGCAG	1260
Db	1201	AAGTAGTATCAGAAATGATCGGACGTCGAAATACCGTAAGAAATGACCGGACGTCGCGCAG	1260
Qy	1261	GTGCACTGAGTTTAACTTGAATAACCGTTAGGCTTGGCTGCTGTTATTAGAGAGCTCA	1320
Db	1261	GTGCACTGAGTTTAACTTGAATAACCGTTAGGCTTGGCTGCTGTTATTAGAGAGCTCA	1320
Qy	1321	CGTAAACATATCTCTCTACTACTACTACTACTACTACTACTACTACTACTACTACTATAA	1380
Db	1321	CGTAAACATATCTCTCTACTACTACTACTACTACTACTACTACTACTACTACTACTATAA	1380
Qy	1381	TATACAGTTTCTCCCTTCTATACATGTTTCCCTCTCCAAAGCGGCTTTTCCACTTGTGA	1440
Db	1381	TATACAGTTTCTCCCTTCTATACATGTTTCCCTCTCCAAAGCGGCTTTTCCACTTGTGA	1440
Qy	1441	AAATGACAACTGCACTGCTTGTCTATTTATCTATATATAAAGGATTAATACTACAAAAA	1500
Db	1441	AAATGACAACTGCACTGCTTGTCTATTTATCTATATATAAAGGATTAATACTACAAAAA	1500
Qy	1501	TATACATATACATCCATTCGGATTTTATAATTCGTATCAATTTTCCCAAGTTTGTGTCGA	1560
Db	1501	TATACATATACATCCATTCGGATTTTATAATTCGTATCAATTTTCCCAAGTTTGTGTCGA	1560
Qy	1561	CTGCGCTTATTTTAACTTGTACGAAAAATAAAAAATTTAAACTCATACTTAAAAATATC	1620
Db	1561	CTGCGCTTATTTTAACTTGTACGAAAAATAAAAAATTTAAACTCATACTTAAAAATATC	1620
Qy	1621	ATGTGCTAAATTAATTTACAGTAAATATAAAAAATTAATTAATTTTGTGATTAAGAC	1680
Db	1621	ATGTGCTAAATTAATTTACAGTAAATATAAAAAATTAATTAATTTTGTGATTAAGAC	1680
Qy	1681	GAGCCAAATTAATTTGAACTTGTAAAGGATTAAGATTAAGATTAAGATTAAGATTAAG	1740
Db	1681	GAGCCAAATTAATTTGAACTTGTAAAGGATTAAGATTAAGATTAAGATTAAGATTAAG	1740
Qy	1741	ACATATCTAAATTAATTTTAAATAATAAAAAACCATGTCGGTCCGCGCGGACACTATTGG	1800
Db	1741	ACATATCTAAATTAATTTTAAATAATAAAAAACCATGTCGGTCCGCGCGGACACTATTGG	1800
Qy	1801	TCGAGAGATAGCCAGACATGCAAGGCTTCACTTTAAATTCGATTTAGTCAAAACCGTGA	1860
Db	1801	TCGAGAGATAGCCAGACATGCAAGGCTTCACTTTAAATTCGATTTAGTCAAAACCGTGA	1860
Qy	1861	AAATTTTAAATTTGCGCGCTGCTTAGGCTGGATATAGCTCATTTGGTTTATCTATAGCTTA	1920
Db	1861	AAATTTTAAATTTGCGCGCTGCTTAGGCTGGATATAGCTCATTTGGTTTATCTATAGCTTA	1920
Qy	1921	TTACATTTCTCTTACCGTCTTAACTTAACTCTCGAGCGGTGAAAGGAGAGAGA	1980
Db	1921	TTACATTTCTCTTACCGTCTTAACTTAACTCTCGAGCGGTGAAAGGAGAGAGA	1980

QY	1981	GAAGAACTTCATCTTCTGATCTCACACACATATCCCATTCGCGCTCAACCAACTGATC	2040
Db	1981	GAAGAACTTCATCTTCTGATCTCACACACATATCCCATTCGCGCTCAACCAACTGATC	2040
QY	2041	TAGAAGTTTAGATCTTGTGTTAAATAACACAGCTTATTTGAACGATGCTCTACTATATAGTA	2100
Db	2041	TAGAAGTTTAGATCTTGTGTTAAATAACACAGCTTATTTGAACGATGCTCTACTATATAGTA	2100
QY	2101	TGTGAAGAACTGTGCAAGCAGTGCAGCAGCACTAGATAGTTAAGAAATAAATACAGATAG	2160
Db	2101	TGTGAAGAACTGTGCAAGCAGTGCAGCAGCACTAGATAGTTAAGAAATAAATACAGATAG	2160
QY	2161	ATAAGAGATAGATAAGCAACAGATATATGTTATAGGATATAGATAGGCAACAGATATATG	2220
Db	2161	ATAAGAGATAGATAAGCAACAGATATATGTTATAGGATATAGATAGGCAACAGATATATG	2220
QY	2221	CACGCTGGCAGAGATAGATATAGATATAGGACAGATAGAGAGAAAATAAATAGCAGAT	2280
Db	2221	CACGCTGGCAGAGATAGATATAGATATAGGACAGATAGAGAGAAAATAAATAGCAGAT	2280
QY	2281	AATATATTAAATATAGATAGATATATCTCACCACATCACTACAGTACACATTCACG	2340
Db	2281	AATATATTAAATATAGATAGATATATCTCACCACATCACTACAGTACACATTCACG	2340
QY	2341	AGTGACCGCGATGCGAGGAGACAAACCGTACACGCGCGCTTGCGAGAACACTTTCC	2400
Db	2341	AGTGACCGCGATGCGAGGAGACAAACCGTACACGCGCGCTTGCGAGAACACTTTCC	2400
QY	2401	AAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTCTCTATTTATGGAGGAGCAGCC	2460
Db	2401	AAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTCTCTATTTATGGAGGAGCAGCC	2460
QY	2461	AGCTACAGCTACACGCGTGGCGAAGCAGACACACGATCACTCACTCTCGCGGCCA	2520
Db	2461	AGCTACAGCTACACGCGTGGCGAAGCAGACACACGATCACTCACTCTCGCGGCCA	2520
QY	2521	TTGTCTCTCTCTGCGTCTCTGCTT 2547	
Db	2521	TTGTCTCTCTCTGCGTCTCTGCTT 2547	

RESULT 2
AAD25704
ID AAD25704 standard; DNA; 1505 BP.
AC AAD25704;
DT 12-MAR-2002 (first entry)
DE Maize glutamine synthetase (GSI-2) gene.
XX Maize; transcription regulatory region; nitrogen metabolism; invertase;
KW glutamine synthetase; seed assimilation; seed development; GSI-2 gene;
KW amino acid transaminase; fungal resistance; disease resistance;
KW carbon metabolism; ds.
OS Zea mays.
FH Key
FT misc_feature 1
FT Location/Qualifiers
FT /tag= a
FT /note= "5', deletion start site"
FT 259
FT misc_feature
FT /tag= b
FT /note= "5', deletion start site"
FT 430..439
FT protein_bind
FT /tag= c
FT /bound_moiety= "c-myb transcription factor"
FT 443..448
FT protein_bind
FT /tag= d
FT /bound_moiety= "NIT2 transcription factor"
FT 459
FT misc_feature

FT				/tag= e
FT	protein_bind			/note= "5', deletion start site"
FT				483..488
FT				/tag= f
FT				/bound_moiety= "NIT2 transcription factor"
FT	CAAT_signal			500..503
FT				/tag= g
FT	misc_feature			593
FT				/tag= h
FT				/note= "5', deletion start site"
FT				603..608
FT				/tag= i
FT	TATA_signal			/note= "P site"
FT				626..631
FT				/tag= j
FT	misc_feature			631
FT				/tag= k
FT				/note= "5', deletion start site"
FT				665..767
FT	5'UTR			/tag= m
FT				665
FT	misc_signal			/tag= l
FT				/note= "Transcription start site"
FT				768..840
FT	exon			/tag= n
FT				/number= 1
FT	intron			841..1222
FT				/tag= o
FT				/number= 1
FT				/cons_splice= (5'site:NO, 3'site:YES)
FT	exon			1223..1262
FT				/tag= p
FT				/number= 2
FT	intron			1263..1469
FT				/tag= q
FT				/number= 2
FT	exon			1470..1505
FT				/tag= r
FT				/number= 3
FT				/partial
XX				
XX				WO200192465-A2.
XX				
PD				06-DEC-2001.
XX				
XX				23-MAY-2001; 2001WO-US010830.
XX				
XX				25-MAY-2000; 2000US-0206984P.
XX				(BIOT-) BIOTECHNOLOGY RES & DEV CORP.
XX				Muhitch MJ;
XX				
XX				WPI; 2002-090042/12.
DR				
XX				
XX				New maize glutamine synthase gene promoter, useful for affecting seed
PT				assimilation and development (e.g. increasing seed yield and quality) in
PT				plants, and for producing plants with increased fungal and disease
PT				resistance.
XX				
XX				Example; Fig 1; 4lpp; English.
XX				
CC				The invention relates to transcription regulatory region (promoter) for
CC				the maize glutamine synthetase (GSI-2) gene. The GSI-2 gene comprising
CC				the transcription regulatory region is useful for affecting seed
CC				assimilation and development, and for increasing fungal and disease
CC				resistance. It is useful for producing plants with reduced mycotoxin
CC				levels and increased disease resistance, and for increasing seed yield
CC				and quality in plants. It is also useful for encoding proteins involved
CC				in seed development and metabolism, particularly enzymes involved in
CC				carbon and/or nitrogen metabolism (e.g. glutamine synthetases or their
CC				isozymes, amino acid transaminases and invertases). The present sequence
CC				is maize GSI-2 gene

PG Pub: 20040148651
— how do I get this?
what IS application #?

```
XX SQ Sequence 1505 BP; 378 A; 394 C; 286 G; 447 T; 0 U; 0 Other;
Query Match 10.0%; Score 254.2; DB 6; Length 1505;
Best Local Similarity 93.6%; Pred. No. 2.2e-45;
Matches 265; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 2265 AAATAAATAGCAGATATATATTAATATAGATAGATATATTTCTACCAATCACTA 2324
DB 449 ATAAAGTATAGAGGCACAGATAGATATAGATATATTTCTACCAATCACTA 508
QY 2325 CAGTACACATTCAGAGTGCAGCGGATGCAGTCGAGAGACACCGTACCGCGGCC 2384
DB 509 CAGTACACATTCAGAGTGCAGCGGATGCAGTCGAGAGACACCGTACCGCGGCC 568
QY 2385 TTGCAGAACACTTTCACGAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTCTAT 2444
DB 569 TTGCAGAACACTTTCACGAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTCTAT 628
QY 2445 TTATGGAGGAGCAGCAGCTACAGGCTACAGCGGTGGCGAAAGCACACCGATCAATCA 2504
DB 629 TTATGGAGGAGCAGCAGCTACAGGCTACAGCGGTGGCGAAAGCACACCGATCAATCA 688
QY 2505 CACTCAGTCGGCGCATTTGCTGCTGCTGCTGCTGCTGCTT 2547
DB 689 CACTCAGTCGGCGCATTTGCTGCTGCTGCTGCTGCTT 731
RESULT 3
AAD25728
ID AAD25728 standard; DNA; 664 BP.
XX AC AAD25728;
XX DT 12-MAR-2002 (first entry)
XX DE Maize glutamine synthetase (GSI-2) gene transcription regulatory region.
XX KW Maize; transcription regulatory region; nitrogen metabolism; invertase;
KW glutamine synthetase; seed assimilation; seed development; GSI-2 gene;
KW amino acid transaminase; fungal resistance; disease resistance;
KW carbon metabolism; ds.
XX OS Zea mays.
XX FH Key Location/Qualifiers
FT protein_bind 430..439
FT /tag= a
FT /bound_moiety= "c-myb transcription factor"
FT protein_bind 443..448
FT /tag= b
FT /bound_moiety= "NIT2 transcription factor"
FT protein_bind 483..488
FT /tag= c
FT /bound_moiety= "NIT2 transcription factor"
FT CAAT_signal 500..503
FT /tag= d
FT misc_feature 603..608
FT /tag= e
FT /note= "p site"
FT TATA_signal 626..631
FT /tag= f
XX WO200192465-A2.
XX PD 06-DEC-2001.
XX PF 23-MAY-2001; 2001WO-US010830.
XX PR 25-MAY-2000; 2000US-0206984P.
XX PA (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
XX
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PI Muhitch MJ;
XX WPI; 2002-090042/12.
XX New maize glutamine synthase gene promoter, useful for affecting seed
PT assimilation and development (e.g. increasing seed yield and quality) in
PT plants, and for producing plants with increased fungal and disease
PT resistance.
XX Claim 1; Fig 2; 41pp; English.
XX The invention relates to transcription regulatory region (promoter) for
CC the maize glutamine synthetase (GSI-2) gene. the GSI-2 gene comprising
CC the transcription regulatory region is useful for affecting seed
CC assimilation and development, and for increasing fungal and disease
CC resistance. It is useful for producing plants with reduced mycotoxin
CC levels and increased disease resistance, and for increasing seed yield
CC and quality in plants. It is also useful for encoding proteins involved
CC in seed development and metabolism, particularly enzymes involved in
CC carbon and/or nitrogen metabolism (e.g. glutamine synthetases or their
CC isozymes, amino acid transaminases and invertases). The present sequence
CC is maize GSI-2 gene transcription regulatory region
XX SQ Sequence 664 BP; 207 A; 142 C; 112 G; 203 T; 0 U; 0 Other;
Query Match 7.4%; Score 188.8; DB 6; Length 664;
Best Local Similarity 92.1%; Pred. No. 3.3e-31;
Matches 199; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 2265 AAATAAATAGCAGATATATTAATATAGATAGATATATTTCTACCAATCACTA 2324
DB 449 ATAAAGTATAGAGGCACAGATAGATATAGATATATTTCTACCAATCACTA 508
QY 2325 CAGTACACATTCAGCAGTGCAGCGGATGCAGTCGAGAGACACCGTACCGCGGCC 2384
DB 509 CAGTACACATTCAGCAGTGCAGCGGATGCAGTCGAGAGACACCGTACCGCGGCC 568
QY 2385 TTGCAGAACACTTTCACGAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTCTAT 2444
DB 569 TTGCAGAACACTTTCACGAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTCTAT 628
QY 2445 TTATGGAGGAGCAGCAGCTACAGGCTACAGCGGTGGCGAAAGCACACCGATCAATCA 2480
DB 629 TTATGGAGGAGCAGCAGCTACAGGCTACAGCGGTGGCGAAAGCACACCGATCAATCA 664
RESULT 4
ADE25029
ID ADE25029 standard; cDNA; 3001 BP.
XX AC ADE25029;
XX DT 29-JAN-2004 (first entry)
XX DE Plant growth associated gene cDNA seq id 4.
XX KW plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis;
KW Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;
KW Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;
KW Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;
KW Quercus; gene; ss.
XX OS Magnoliophyta.
XX PN US2003188343-A1.
XX PD 02-OCT-2003.
XX PF 07-JAN-2003; 2003US-00338777.
XX PR 09-JAN-2002; 2002US-0347288P.
XX PA (LYNX-) LYNX THERAPEUTICS INC.
```

XX Bowen BA, Haudenschild CD, Buckler ES;
PI WPI: 2003-803305/75.
DR P-PSDB; ADE25059.
XX New isolated or recombinant polypeptide for use in modulating a plant
PT growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or
PT Oryza.
XX Claim 1; SEQ ID NO 4; 81pp; English.
XX The invention describes an isolated or recombinant polypeptide (I)
CC comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in
CC the specification, or a conservative variant; (b) encoded by 1 of 30
CC sequences (S2), as given in the specification, or a conservative variant;
CC (c) encoded by a sequence that hybridises under stringent conditions to
CC S2; and (d) encoded by a sequence 70 % identical to S2. The expression or
CC activity of (I) is modulated to modulate a plant growth trait in a
CC flowering plant, of the family Brassicaceae, preferably in a plant that
CC is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum,
CC Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum,
CC Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,
CC Pinus, or Quercus. A new method is used to detect genes for a plant
CC growth trait. This sequence represents a plant growth associated cDNA.
XX
SQ Sequence 3001 BP; 836 A; 566 C; 538 G; 1061 T; 0 U; 0 Other;

Query Match 4.2%; Score 107.2; DB 10; Length 3001;
Best Local Similarity 62.2%; Pred. No. 4e-13;
Matches 194; Conservative 0; Mismatches 103; Indels 15; Gaps 1;
QY 102 AGGTTCGGGATTGACGAGGATACACCTTCTCCAGAGGACACCAAGTGGCTCTCGGT 161
Db 1447 AGGTATGGAAATCGAACAAGATACACTTTGTTCAGAGGAGTGAACTGGCCCTTTGGA 1506
QY 162 TGGCGCTGGGGCTGACCTGGCCCTCAGGTAGATTAGATGGATCTGCGTGCCTCCAGG 221
Db 1507 TGGCCCATTTGGTGTCTCCCTGGCCCTCAGGTATACGTTTTCGGAGTTTTCGT 1566
QY 222 CTCAGCCATATCGATGGCTTTGATCAGCTGACGGAATG-----ATCCTG 266
Db 1567 TTGTTTACTGCTCTTTTTCGATTCCTCGTTCCTTGTGCTTCTGAAATATCTTTGCACTCTT 1626
QY 267 GCAGGACCTTACTACTGCGCGTCCGAGCGGACCAAGTCCCTACGCGCGGACATCGTGA 326
Db 1627 GCAGGACCATCTACTACTGATTTGGAGCTGACAAATCTTTTGAAGACATTTGTTGA 1686
QY 327 CGCGCACTACAAGGCTGCTCTACGCGGCAATCGACATCAGTGGCATCAACGGGGAGGT 386
Db 1687 TGCTCACTACAAGGCTCTTTGTATGCTGGAATCAACATCAGTGGGATCAATGGAGAAGT 1746
QY 387 CATGCCGGGGCA 398
Db 1747 CATGCCGGGACA 1758

RESULT 5
ADK54422
ID ADK54422 standard; DNA; 599 BP.
XX
AC ADK54422;
XX
DT 06-MAY-2004 (first entry)
XX
DE Plant DNA sequence which confers altered metabolic characteristic #1805.
XX altered metabolic characteristic; plant; acid metabolism;
KW alcohol metabolism; fatty acid metabolism;
KW branched fatty acid metabolism; alkaloid metabolism;
KW amino acid metabolism; ester metabolism; glyceride metabolism;
KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;
KW terpene metabolism; isoprenoid metabolism; alkene metabolism;

KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX Unidentified.
OS
XX WO2003020936-A1.
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027884.
XX
XX 31-AUG-2001; 2001US-0316471P.
XX (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX WPI; 2003-313091/30.
XX Novel genes that confer altered metabolic characteristics in Nicotiana
PT benchamiana plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX
PS Claim 1; SEQ ID NO 1805; 2576pp; English.
XX
CC The invention comprises DNA sequences which confer an altered metabolic
CC characteristic when they are expressed in a plant. The DNA sequences of
CC the invention are useful for producing plants with an altered metabolic
CC characteristic, such as: altered acid metabolism, alcohol metabolism,
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
CC base metabolism, altered amino acid metabolism, altered ester metabolism,
CC altered glyceride metabolism, altered phenolic metabolism, altered
CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene
CC shuffling or sexual PCR procedures. The present nucleic acid represents a
CC DNA sequence of the invention.

Query Match 4.1%; Score 103.2; DB 10; Length 599;
Best Local Similarity 86.4%; Pred. No. 1.7e-12;
Matches 114; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 268 CAGGACCTTACTACTGCGCTCGGAGCGGACCAAGTCTTACGGCGGGACATCGTGGAC 327
Db 271 CAGGACCATCTACTGCGCTCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 330
QY 328 CGGCACTACAAGGCTGCTCTACGCGGCAATCGACATCAGTGGCATCAACGGGGAGTGC 387
Db 331 GCCCACTACAAGGCTGCTCTACGCGGCAATCGACATCAGTGGCATCAACGGGGAGTGC 390
QY 388 ATGCCGGGGCAG 399
Db 391 ATGCCGGGGCAG 402

RESULT 6
ADD17903
ID ADD17903 standard; DNA; 863 BP.
XX
AC ADD17903;
XX
DT 15-JAN-2004 (first entry)
XX
DE DNA (SeqID 1971) that confers an altered visual phenotype in plants.
XX ds; visual phenotype; plant; architecture; leaf surface; chlorotic;
KW bleaching; etching; wet leaf; stunting; elongation; texture;
KW agronomic trait; growth regulation; dwarf variety; insect resistance;

DE Gene encoding glutamine synthase in cytosol of rice plant roots.

KW Herbicide-resistance; RGS; ss.

XX Oryza sativa.

XX Key Location/Qualifiers
 FH CDS 59..1132
 FT /*tag= a
 FT /product= "RGS"

XX JP02182190-A.

XX 16-JUL-1990.

XX 16-JUN-1989; 89JP-00154157.

XX 09-SEP-1988; 88JP-00225816.

XX (MITU) MITSUBISHI KASEI CORP.

XX (MITS) MITSUBISHI CORE.

XX (MITS) MITSUBISHI CORP.

XX WPI; 1990-258259/34.

XX P-PSDB; AAR06492.

DE Gene to encode glutamine synthetase - is in cytosol of rice plant leaves and is used for formation of herbicide-resistant plants.

XX Claim 4; Page 3; 16pp; Japanese.

XX The gene was sequenced from a clone isolated from a cDNA library prepd. from the cytosol of rice plant roots. It is useful for the development of herbicide-resistant plants and in the analysis of mechanism of induction by light or gibberellin, and also for analysis of tissue specificity. The protein encoded by the gene is designated RGS and is one of three similar proteins, the others being RGLI (from leaf cytosol) and RGLC (from leaf chloroplasts). See also AAQ05727 and AAQ02729. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1200 BP; 287 A; 364 C; 348 G; 201 T; 0 U; 0 Other;

Query Match 4.1%; Score 103.2; DB 2; Length 1200;

Best Local Similarity 86.4%; Pred. No. 2.2e-12;

Matches 114; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 268 CAGGACCTTACTTACTGCGCTCGGAGGACAGTCTACGGCGGACATCGTGAC 327

Db 518 CAGGAGACCATACTACTGCGCTCGGAGGAGGCTTCCGCGCGGACATCGTGAC 577

QY 328 GGCACCTACAAGCGCTGCTCTACCGCGGACATCAGTGCCATCAACGGGGAGGTC 387

Db 578 GCCCACTACAAGCGCTGCTCTACCGCGGACATCAGTGCCATCAACGGGGAGGTC 637

QY 388 ATGCCGGGCGCAG 399

Db 638 ATGCCGGGCGCAG 649

RESULT 9

ADSG9423

ID ADSG9423 standard; cDNA; 281 BP.

XX ADSG9423;

XX 18-NOV-2004 (first entry)

XX Corn seedling-derived polynucleotide (cpds), SEQ ID 4439.

XX Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth; seed development; disease resistance; insect infestation; fungal disease; Bacterial infection; Goss' Bacterial wilt; blight; Stewart's bacterial wilt; Holcus spot; bacterial leaf blight; leaf spot;

KW bacterial stripe; maize dwarf mosaic virus infection; environmental stress; water stress; pH stress; temperature stress; pollution; injury; pesticide.

XX Zea mays.

XX US2003237110-A9.

XX 25-DEC-2003.

XX 06-AUG-2001; 2001US-00923876.

XX 12-MAY-1998; 98US-0085331P.

XX 21-APR-1999; 99US-00298329.

XX (INCY-) INCYTE PHARM INC.

XX Laigudi RV, Ito LY, Sherman BK;

XX WPI; 2002-195165/25.

XX New corn seedling-derived polynucleotides and polypeptides, useful in identifying and altering desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield.

XX Claim 1; SEQ ID NO 4439; 33pp; English.

XX The invention relates to a corn seedling-derived polynucleotide (cdp) selected from ADS64985-ADS71316, or their complements and fragments. Also included are a composition for the detection of altered expression of a cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a method of detecting a polynucleotide in a biological sample using a cdp, a method for using oligomers (and amplification) to recover a regulatory element from a DNA library using oligomers designed against a cdp, a seedling specific regulatory element that regulates the expression of a cdp, an expression vector containing a cdp or regulatory element, a plant transformed with the vector, a host cell containing the vector (and expressing a corn seedling derived protein, CDP), an anti-CDP antibody, identifying a compound which binds a CDP and screening a plurality of compounds for binding to cdp polynucleotide. The cdp polynucleotides, proteins, vectors, cells and antibodies are useful for the identification, evaluation and alteration of seed growth and development, disease resistance (e.g. to insect infestation, fungal disease, bacterial infection, Goss' Bacterial wilt, blight, Stewart's bacterial wilt, Holcus spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf mosaic virus infection) and resistance to environmental stresses (e.g. water stress, pH stress, temperature stress, pollution, injury or pesticides). The present sequence is cdp cDNA sequence.

XX Sequence 281 BP; 54 A; 81 C; 88 G; 56 T; 0 U; 2 Other;

Query Match 4.0%; Score 101; DB 7; Length 281;

Best Local Similarity 85.0%; Pred. No. 3.9e-12;

Matches 113; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 268 CAGGACCTTACTTACTGCGCTCGGAGGACAGTCTACGGCGGACATCGTGAC 327

Db 106 CAGGTCCTTACTTACTGCGCTCGGAGGAGTCTCGGCGGACATCGTGAC 165

QY 328 GCGCACTACAAGCGCTGCTCTACCGCGGACATCAGTGCCATCAACGGGGAGGTC 387

Db 166 GCCCACTACAAGCGCTGCTCTACCGAGGACATCAGTGCCATCAACGGGGAGGTC 225

QY 388 ATGCCGGGCGCAG 400

Db 226 ATGCCGGGCGCAG 238

RESULT 10

ADJ44656

ID ADJ44656 standard; cDNA; 693 BP.

XX

AC ADJ44656;
XX 06-MAY-2004 (first entry)
XX Plant cDNA #5656.
XX
KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.
XX
OS Eukaryota.
XX
XX US2004016025-A1.
XX
XX 22-JAN-2004.
XX
XX 26-SEP-2002; 2002US-00260238.
XX
XX 26-SEP-2001; 2001US-0325277P.
XX 26-SEP-2001; 2001US-0325448P.
XX 04-APR-2002; 2002US-0370620P.
XX
XX (BUDW/) BUDWORTH P.
XX (MOUG/) MOUGHAMER T.
XX (BRIG/) BRIGGS S P.
XX (COOP/) COOPER B.
XX (GLAZ/) GLAZEBROOK J.
XX (GOFF/) GOFF S A.
XX (KATA/) KATAGIRI F.
XX (KREP/) KREPS J.
XX (PROV/) PROVANT N.
XX (RICK/) RICHE D.
XX (ZHUT/) ZHU T.
XX
XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
XX Goff SA, Katagiri F, Kreps J, Provant N, Ricke D, Zhu T;
XX WPI; 2004-190374/18.
XX
XX New rice promoter, useful for manipulating crop plants to alter or
XX improve phenotypic characteristics, e.g. produce large quantities of oil
XX or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX or high nutritional value.
XX
XX Example 13; SEQ ID NO 5656; 230pp; English.
XX
XX The invention relates to plant nucleotide sequences that direct seed-,
XX leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
XX or constitutive transcription of an operatively linked nucleic acid
XX segment. The invention also relates to a method for augmenting a plant
XX genome and a method of identifying a gene, where its expression is
XX altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX sorghum, rice or wheat. The polynucleotides and the polypeptides they
XX encode are useful for manipulating crop plants to alter or improve
XX phenotypic characteristics, to produce large quantities of oil or
XX proteins, to incur resistance to insecticides, viruses or fungi, and to
XX incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
XX have a high nutritional value with reduced apical dominance or dwarfism,
XX early flowering or altered metabolic pathways. This sequence represents a
XX plant nucleic acid of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification but was obtained in
XX electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 693 BP; 140 A; 211 C; 236 G; 106 T; 0 U; 0 Other;
XX
XX Query Match 3.9%; Score 98.6; DB 12; Length 693;
XX Best Local Similarity 74.0%; Pred. No. 1.8e-11;
XX Matches 125; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

OY 270 GGGACCTTACTACTGCGCCCTCGGAGCGGACAAGTCTCTACGGCGGACATCGTGGACGC 329
DB 87 GGGTCCTTACTACTGTGGAATCGCGCCGAAAGTCTGTCGCGCGACATCGTGGACGC 146
OY 330 GCACTACAAGGCTGCTCTACCGCGCATCGACATCAGTGGCATCAACGGGAGGTGAT 389
DB 147 CCACTACAAGGCTGCTGTTATCGGGCATCAACATCAGTGGCATCAACGGGAGGTGAT 206
OY 390 GCGCGGCGAGGTGACAGCGTCTGCTCTAGCTACCTTCTTTAACTGCA 438
DB 207 GCCAGGCGAGTGGGAGTTCCAAAGTCGGGCGCTTCGTCGGGTATTTCTTCA 255

RESULT 11
ADJ40037
ID ADJ40037 standard; cDNA; 1273 BP.
XX
XX AC ADJ40037;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Plant cDNA #1037.
XX
XX KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
XX KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
XX KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
XX KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
XX KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX KW antifungal.
XX
XX OS Eukaryota.
XX
XX US2004016025-A1.
XX
XX 22-JAN-2004.
XX
XX 26-SEP-2002; 2002US-00260238.
XX
XX 26-SEP-2001; 2001US-0325277P.
XX 26-SEP-2001; 2001US-0325448P.
XX 04-APR-2002; 2002US-0370620P.
XX
XX (BUDW/) BUDWORTH P.
XX (MOUG/) MOUGHAMER T.
XX (BRIG/) BRIGGS S P.
XX (COOP/) COOPER B.
XX (GLAZ/) GLAZEBROOK J.
XX (GOFF/) GOFF S A.
XX (KATA/) KATAGIRI F.
XX (KREP/) KREPS J.
XX (PROV/) PROVANT N.
XX (RICK/) RICHE D.
XX (ZHUT/) ZHU T.
XX
XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
XX Goff SA, Katagiri F, Kreps J, Provant N, Ricke D, Zhu T;
XX WPI; 2004-190374/18.
XX
XX New rice promoter, useful for manipulating crop plants to alter or
XX improve phenotypic characteristics, e.g. produce large quantities of oil
XX or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX or high nutritional value.

CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
 CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
 CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
 CC encode are useful for manipulating crop plants to alter or improve
 CC phenotypic characteristics, to produce large quantities of oil or
 CC proteins, to incur resistance to insecticides, viruses or fungi, and to
 CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
 CC have a high nutritional value with reduced apical dominance or dwarfism,
 CC early flowering or altered metabolic pathways. This sequence represents a
 CC plant nucleic acid of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1273 BP; 277 A; 355 C; 377 G; 261 T; 0 U; 3 Other;

Query Match 3.8%; Score 96.8; DB 12; Length 1273;
 Best Local Similarity 76.8%; Pred. No. 5.6e-11;
 Matches 116; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
 QY 263 CTTGGCAGGGACCTTACTACTCGCGCTGCGAGCGGACAAAGTCTTACGGCGGGACATCG 322
 DB 492 CCTCAGAGGGTCCGTACTACTGTGCGGCGNGGCCNATATATCGTACGGCGGACATCG 551
 QY 323 TGGACGGGCACTAACAGGCTGCTTACGCGCGCATCGACATCATGTCGATCAACGGGG 382
 DB 552 TTGATGCCCACTACAAAGGCTGCTTGTTCGCGCATCAACATCAGCGGGATCAACGCAG 611
 QY 383 AGGTCATCGCGGGCGAGGTACAGCGTGTGC 413
 DB 612 AAGTCATCGCGGGCGAGGTGAGGTCC 642

RESULT 12
 ADD17881/c
 ID ADD17881 standard; DNA; 1211 BP.
 XX
 AC ADD17881;
 XX
 XX 15-JAN-2004 (first entry)
 XX
 DE DNA (SeqID 1949) that confers an altered visual phenotype in plants.
 XX
 KW ds; visual phenotype; plant; architecture; leaf surface; chlorotic;
 KW bleaching; etching; wet leaf; stunting; elongation; texture;
 KW agronomic trait; growth regulation; dwarf variety; insect resistance;
 KW heat stress; transgenic.
 XX
 OS Unidentified.
 XX
 PN WO2003020741-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 30-AUG-2002; 2002WO-US027880.
 XX
 PR 31-AUG-2001; 2001US-0316326P.
 XX
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 XX
 PI Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;
 XX
 DR WPI; 2003-300858/29.
 XX
 PT Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
 PT sativa, Saccharum cerevisiae, and Papaver rhoeas, useful for
 PT conferring altered visual phenotypes in plants.
 XX
 PS Claim 1; SEQ ID NO 1949; 517pp; English.
 XX

CC This invention relates to the identification and isolation of novel
 CC nucleic acid molecules that confer altered visual phenotypes in plants.
 CC Specifically, it refers to modifications of plant architecture and/or

CC leaf surface features in plants, such as chlorotic, bleaching, etching,
 CC wet leaf, stunting, elongation and texture phenotypes, which are thought
 CC will be agronomic traits beneficial to the farmer. As such, these novel
 CC phenotypes can affect growth regulation i.e. useful for creating dwarf
 CC varieties, exhibit resistance to insects or heat stress, confer changes
 CC in pigment content such that plants have enhanced vitamin production or
 CC delayed senescence and also for example produce plants that control the
 CC production of ethylene. Furthermore, the present invention comprises
 CC generating transgenic plants, as well as reproducibly altering the visual
 CC phenotype of plant seeds, plant tissues and plant cells containing the
 CC polynucleotides described herein. This polynucleotide is a homologue of a
 CC DNA sequence that confers an altered visual phenotype when expressed in
 CC plants, the method of the invention.
 XX

SQ Sequence 1211 BP; 237 A; 333 C; 363 G; 278 T; 0 U; 0 Other;
 Query Match 3.7%; Score 95.2; DB 10; Length 1211;
 Best Local Similarity 82.6%; Pred. No. 1.2e-10;
 Matches 109; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 268 CAGGGACCTTACTACTGCGCGTGGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 327
 DB 758 CAGGCTCTTACTACTGTGTATCGTGTCTGACAAAGTCTTTGGCGGTATTTGTTGAC 699
 QY 328 GCGCACTACAAAGGCTGCTTACGCGCGCATCGACATCATGTCGAGGAGGTC 387
 DB 698 TCCCACTACAAGGCTTGCTCTATGCGCGCATCAACATCAGTGGATCAACGGCGAGTTC 639
 QY 388 ATGCGGGGCGAG 399
 DB 638 ATGCCAGGACAG 627

RESULT 13
 ADK54420
 ID ADK54420 standard; DNA; 1211 BP.
 XX
 AC ADK54420;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Plant DNA sequence which confers altered metabolic characteristic #1803.
 XX
 KW altered metabolic characteristic; plant; acid metabolism;
 KW alcohol metabolism; fatty acid metabolism;
 KW branched fatty acid metabolism; alkaloid metabolism;
 KW amino acid metabolism; ester metabolism; glyceride metabolism;
 KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
 KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
 XX
 OS Unidentified.
 XX
 PN WO2003020936-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 30-AUG-2002; 2002WO-US027884.
 XX
 PR 31-AUG-2001; 2001US-0316471P.
 XX
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 XX
 PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
 PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
 XX
 DR WPI; 2003-313091/30.
 XX
 PT Novel genes that confer altered metabolic characteristics in Nicotiana
 PT benthamiana plants, useful for altering the levels of metabolites e.g.
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

XX PS Claim 1; SEQ ID NO 1803; 2576pp; English.

XX CC The invention comprises DNA sequences which confer an altered metabolic

XX CC characteristic when they are expressed in a plant. The DNA sequences of

XX CC the invention are useful for producing plants with an altered metabolic

XX CC characteristic, such as: altered acid metabolism, alcohol metabolism,

XX CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other

XX CC base metabolism, altered amino acid metabolism, altered ester metabolism,

XX CC altered glyceride metabolism, altered phenolic metabolism, altered

XX CC carbohydrate metabolism, altered sterol, oxygenated terpene, or

XX CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon

XX CC metabolism, ketone or quinone metabolism. The DNA sequences of the

XX CC invention may be used to provide disease resistance in a plant and gene

XX CC shuffling or sexual PCR procedures. The present nucleic acid represents a

XX CC DNA sequence of the invention.

XX SQ Sequence 1211 BP; 278 A; 363 C; 333 G; 237 T; 0 U; 0 Other;

Query Match 3.7%; Score 95.2; DB 10; Length 1211;

Best Local Similarity 82.6%; Pred. No. 1.2e-10;

Matches 109; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTGCGCGTTCGAGCGGACAAAGTCTTACGCGGACATCGTGAC 327

Db 454 CAGGTCCTTACTACTGTGATCGGTCTGACAAAGTCTTTTGGCGGTGATATTGTTGAC 513

Qy 328 CGCAGCTACAAGCGCTGCTTACGCGGCGATCGACATCAGTGGCATCAACGGGGAGGTC 387

Db 514 TCCCACTACAAGGCTTGCTCTATGCGGCGCATCAACATCAGTGGAAATCAACGGCGAGGTC 573

Qy 388 ATGCCGGGGCAG 399

Db 574 ATGCCAGGACAG 585

RESULT 14

AAQ05727

ID AAQ05727 standard; cDNA; 1255 BP.

XX AC AAQ05727;

XX DT 25-MAR-2003 (revised)

XX DT 02-JAN-1991 (first entry)

XX DE Gene encoding glutamine synthase in cytosol of rice plant leaves.

XX KW Herbicide-resistance; RGSLLI; ss.

XX OS Oryza sativa.

XX FH Key Location/Qualifiers

XX FT CDS 55..1125

XX FT /*tag= a

XX FT /product= "RGSLLI"

XX FT

XX JPO2182190-A.

XX PN 16-JUL-1990.

XX PD 16-JUN-1989; 85JP-00154157.

XX PF 09-SEP-1988; 89JP-00225816.

XX PR (MITU) MITSUBISHI KASEI CORP.

XX PA (MITS) MITSUBISHI CORE.

XX PA (MITS) MITSUBISHI CORP.

XX DR WPI; 1990-258259/34.

XX DR P-PSDB; AAR06491.

XX PT Gene to encode glutamine synthetase - is in cytosol of rice plant

XX PT leaves and is used for formation of herbicide-resistant plants.

XX PS Claim 2; Page 2; 16pp; Japanese.

XX CC The gene was sequenced from a clone isolated from a cDNA library prepd.

XX CC from the cytosol of rice plant leaves. It is useful for the development

XX CC of herbicide-resistant plants and in the analysis of mechanism of

XX CC induction by light or gibberellin , and also for analysis of tissue

XX CC specificity. The protein encoded by the gene is designated RGSLLI and is

XX CC one of three similar proteins, the others being RGSR (from root cytosol)

XX CC and RGSCL (from leaf chloroplasts). See also AAQ05728 and AAQ02729.

XX CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 1255 BP; 275 A; 390 C; 335 G; 255 T; 0 U; 0 Other;

Query Match 3.7%; Score 95.2; DB 2; Length 1255;

Best Local Similarity 82.6%; Pred. No. 1.2e-10;

Matches 109; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTGCGCGTTCGAGCGGACAAAGTCTTACGCGGCGGACATCGTGAC 327

Db 514 CAGGTCCTTACTACTGTGATCGGTCTGACAAAGTCTTTTGGCGGTGATATTGTTGAC 573

Qy 328 GCGCACTACAAGCGCTGCTTACGCGGCGATCGACATCAGTGGCATCAACGGGGAGGTC 387

Db 574 TCCCACTACAAGGCTTGCTCTATGCGGCGCATCAACATCAGTGGAAATCAACGGCGAGGTC 633

Qy 388 ATGCCGGGGCAG 399

Db 634 ATGCCAGGACAG 645

RESULT 15

AAAN71244

ID AAAN71244 standard; DNA; 4464 BP.

XX AC AAAN71244;

XX DT 25-MAR-2003 (revised)

XX DT 06-JUN-1991 (first entry)

XX DE Genomic sequence of alfalfa coding for glutamine synthetase (GS).

XX KW Herbicide-resistant plant cell; Ti plasmid; Agrobacterium tumefaciens;

XX KW phosphinothrican-resistant; enzyme; ss.

XX OS Medicago sativa.

XX FH Key Location/Qualifiers

XX FT repeat_unit 508..521

XX FT /*tag= m

XX FT repeat_unit 541..554

XX FT /*tag= n

XX FT TATA_signal 589..596

XX FT /*tag= o

XX FT misc_RNA 621..740

XX FT /*tag= q

XX FT exon 741..814

XX FT /*tag= a

XX FT exon 1529..1568

XX FT /*tag= b

XX FT exon 1683..1785

XX FT /*tag= c

XX FT exon 2000..2048

XX FT /*tag= d

XX FT exon 2494..2600

XX FT /*tag= e

XX FT exon 2694..2780

XX FT /*tag= f

XX FT exon 3088..3196

XX FT /*tag= g

XX FT exon 3311..3385

XX FT /*tag= h

XX FT exon 3514..3567

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FT      exon      /*tag= i
FT      3703..3740 /*tag= j
FT      exon      /*tag= j
FT      3831..3990 /*tag= k
FT      exon      /*tag= l
FT      4168..4320 /*tag= l
FT      misc_RNA   /*tag= r
FT      4321..4530 /*tag= r
FT      polyA_site 4527..4530
FT      /*tag= p
XX      W08705327-A.
XX      PD
XX      11-SEP-1987.
XX      PF      27-FEB-1987; 87WO-US000394.
XX      XX
XX      PR      27-FEB-1986; 86US-00833156.
XX      XX
XX      PA      (GEHO ) GEN HOSPITAL CORP.
XX      PI      Goodman HM, Donn G;
XX      DR      WPI; 1987-264124/37.
XX      DR      P-PSDB; AAP71066.
XX      PT      Herbicide-resistant plant cells - contg. DNA sequence combination coding
XX      PT      for over-prodn. of glutamine synthetase.
XX      PS      Claim 21; Fig 4; 49pp; English.
XX      CC      The patent application claims plant cells which contain a combination of:
XX      CC      (a) a genetic sequence coding for genomic GS functional in the plant cell
XX      CC      ; operably linked to: (b) a genetic sequence capable of increasing the
XX      CC      levels of expression of GS. The combination is integrated in the genome
XX      CC      of the plant cell, esp. using a tumour-inducing (Ti) plasmid of
XX      CC      Agrobacterium tumefaciens as vector, e.g. pGV3850. (Updated on 25-MAR-
XX      CC      2003 to correct PA field.)
XX      SQ      Sequence 4464 BP; 1307 A; 683 C; 756 G; 1718 T; 0 U; 0 Other;

Query Match      3.6%; Score 92.8; DB 1; Length 4464;
Best Local Similarity 59.0%; Pred. No. 6.5e-10;
Matches 196; Conservative 0; Mismatches 132; Indels 4; Gaps 2;

QY      269 AGGGACCTTACTACTGCGCGCTCGGAGCGGACAAAGTCTCTACGGCGGGACATCGTGGACG 328
DB      2976 AGGGACCATATATTGTGGAGCTGCTGTGCAAGGCATTTGGCCGTGACATTTGTGACT 3035
QY      329 CGCACTACAAGCCCTGCTCTACGCCGCGCATCGACATCAGTGGCATCAACGGGAGGTCA 388
DB      3036 CACATTACAAGCCCTGCTTTATGCGGCATCAACATCAGTGGAAATCAATGGTGAAGTGA 3095
QY      389 TGCCGGGGCAGGTACAGCGTGTGCTCTAGCTACCTTGTCTTTAACTGCACACTGCACCTC 448
DB      3096 TGCCCTGGTCAAGTAAGTGGACTTATTTACCCCTTTAGCAATTTATTTACTACATTTT 3155
QY      449 TGCACACTGCACAGCTAGTAGTATGCTGTATCTCT---GCTGACCCAGGCTTGTTCGTG 505
DB      3156 TTCAATTTAAATTAACATATGCTGTGATTTTATAAGATTTAAATCTATTGTTTTTTAA 3215
QY      506 GACAGTGGGAGTCCAGGTTCGGCCCTCGCGCGGCTCTCGCGCGGCGA-CAGCTTGGGT 564
DB      3216 TGTAGTGGGAATCCAAAGTTGGTCCCTCAGTTGGTATCTCTGCTGGTATGAGATATGGG 3275
QY      565 GGGCTCGGTACTTCTTGGAGAAACGGGTAGA 596
DB      3276 TTGCTCGTTACATTTTGGAGGTAGGTGGACA 3307
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Searched: 4708233 seqs, 24227607955 residues

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Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_by.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254.2	10.0	1505	AF359511	AF359511 Zea mays
C 2	127.2	5.0	78874	AB018107	AB018107 Arabidops
C 3	123	4.8	143681	AC082645	AC082645 Oryza sat
4	122.6	4.8	1369	ZMGS12	X65927 Z mays mRNA
5	118.8	4.7	74968	AB019230	AB019230 Arabidops
6	118.4	4.6	6652	AB037664	AB037664 Oryza sat
C 7	118.4	4.6	161531	AF004880	AF004880 Oryza sat
8	112.2	4.4	1397	AC148968	AY491968 Triticum
C 9	112	4.4	91634	2 AC148968	AC148968 Medicago
C 10	109.8	4.3	50641	8 AB008270	AB008270 Arabidops
11	108	4.2	3341	8 AY491969	AY491969 Triticum
C 12	108	4.2	146568	8 AC105364	AC105364 Oryza sat
C 13	107.2	4.2	90248	8 AC026480	AC026480 Arabidops
14	104.8	4.1	1299	8 AY491970	AY491970 Triticum
15	104.8	4.1	1490	8 ZMGS14	X65929 Z mays mRNA
16	103.4	4.1	5232	8 BNA271909	AJ271909 Brassica
17	103.2	4.1	1019	8 AY339214	AY339214 Zea mays
18	103.2	4.1	1169	8 OSRIGS8	X14244 Oryza sativ
19	103.2	4.1	1200	6 E02507	E02507 DNA encodin

20	103.2	4.1	1359	8 ZMGS11	X65926 Z.mays mRNA
21	103.2	4.1	1416	8 MZEGS1D	D14579 Zea mays mR
22	103.2	4.1	1422	8 MZEGS1A	D14576 Zea mays mR
23	102.2	4.0	832	8 AB162423	AB162423 Phyllost
24	102.2	4.0	1350	8 MZEGS1B	D14577 Zea mays mR
25	101.6	4.0	695	8 AB125110	AB125110 Brassica
26	101.6	4.0	1278	8 AY491971	AY491971 Triticum
27	101.4	4.0	7498	8 AB015045	AB015045 Arabidops
28	101.4	4.0	63989	8 AB013393	AB013393 Arabidops
29	100.6	3.9	1317	8 ZMGS13	X65928 Z.mays mRNA
30	96.8	3.8	895	8 ZMGS15	X65930 Z.mays mRNA
31	96.8	3.8	1433	8 MZEGS1C	D14578 Zea mays mR
32	95.2	3.7	1255	6 E02506	E02506 DNA encodin
33	95.2	3.7	1275	8 AB037595	AB037595 Oryza sat
34	95.2	3.7	1276	8 AK061157	AK061157 Oryza sat
35	95.2	3.7	1427	8 AK071969	AK071969 Oryza sat
36	95.2	3.7	1457	8 AK099290	AK099290 Oryza sat
37	95.2	3.7	1494	8 AK063913	AK063913 Oryza sat
38	95.2	3.7	1538	8 AK104987	AK104987 Oryza sat
39	95.2	3.7	1553	8 OSSIGS28	X14245 Oryza sativ
40	95.2	3.7	1556	8 AK109397	AK109397 Oryza sat
41	94	3.7	176965	2 AC148164	AC148164 Zea mays
42	92.8	3.6	4464	8 HSGLNAG	X03931 Medicago sa
43	92	3.6	1625	5 BC064185	BC064185 Xenopus t
44	91.4	3.6	160351	2 AC148152	AC148152 Zea mays
45	90.6	3.6	208685	2 AC145726	AC145726 Zea mays

ALIGNMENTS

RESULT 1
AF359511
LOCUS AF359511
DEFINITION Zea mays glutamine synthetase (gs1-2) gene, partial cds.
ACCESSION AF359511
VERSION AF359511.1
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays

1505 bp DNA linear
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1505)
AUTHORS Muhitch,M.J., Liang,H., Rastogi,R. and Sollenberger,K.G.
TITLE Isolation of a promoter sequence from the glutamine synthetase 1-2
gene capable of conferring tissue-specific gene expression in

transgenic maize
Plant Sci. 163 (4), 865-872 (2002)
2 (bases 1 to 1505)
AUTHORS Muhitch,M.J., Liang,H., Rastogi,R. and Sollenberger,K.G.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2001) Mycotoxin Research Unit, NCAUR, ARS, USDA,
1815 N. University St., Peoria, IL 61604, USA

FEATURES
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1. .1505
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/mol_type="genomic DNA"
/variety="B73"
/db_xref="taxon:4577"
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626. .631
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filing date 11-20-2001

not
Pub 15-11-01
Cui 11-06-01
Jett

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ORIGIN
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Best Local Similarity 93.6%; Pred. No. 7.5e-41;
Matches 265; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 2265 AAAATAAATACAGATATATATTAATATAGATAGATATATTTCTACCAATCACTA 2324
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Db 449 ATRAGTATAGAGCAGACAGATAGATATAGATAGATATTTCTACCAATCACTA 508

Qy 2325 CAGTACAACTTCACGAGTGACCGCGGATGACGATCGAGAGGACAAACCGTACCA 2384
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Db 509 CAGTACAACTTCACGAGTGACCGCGGATGACGATCGAGAGGACAAACCGTACCA 568

Qy 2385 TTGCAGACACTTTCACGAGTGACCGCGGATGACGATCGAGAGGACAAACCGTACCA 2444
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Db 569 TTGCAGACACTTTCACGAGTGACCGCGGATGACGATCGAGAGGACAAACCGTACCA 628

Qy 2445 TTATGGAGGACGACGACGCTACAGCTACAGCCGCTGGCGAAAGCACACACGATCA 2504
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Db 629 TTATGGAGGACGACGACGCTACAGCTACAGCCGCTGGCGAAAGCACACACGATCA 688

Qy 2505 CACTCACTCGCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2547
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Db 689 CACTCACTCGCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731

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RESULT 2
AB018107/c
LOCUS      AB018107.1 78874 bp DNA linear PLN 14-FEB-2004
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K12B20.
ACCESSION AB018107 BA000015
VERSION   AB018107.1 GI:3702722
KEYWORDS
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 Kaneko, T., Katoh, T., Sato, S., Nakamura, Y., Asamizu, E., Kotani, H.,
            Miyajima, N. and Tabata, S.
            Structural analysis of Arabidopsis thaliana chromosome 5. IX.
            Sequence features of the regions of 1,011,550 bp covered by
            seventeen P1 and TAC clones
            DNA Res. 6 (3), 183-195 (1999)
JOURNAL   99397451
MEDLINE   10470850
REFERENCE 2 (bases 1 to 78874)
AUTHORS   Nakamura, Y.
TITLE     Direct Submission
JOURNAL   Submitted (08-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research
            Institute, Department of Plant Gene Research; 1532-3, Yana,
            Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,
            Tel: 81-438-52-3935, Fax: 81-438-52-3934)
COMMENT   Address for correspondence: kaos@kazusa.or.jp
            For the latest information on annotation of this clone, please see
            http://www.kazusa.or.jp/kaos/cgi-bin/agg_graph.cgi?c=K12B20
            Genes with similarity to proteins in the databases are described in
            'product' or 'note' qualifiers. Genes that have no significant
            protein similarity are described as 'unknown protein'.
            The software programs used to predict genes include: Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/Grail-1.3/),
            GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
            NetGene2 (S.N. Hebsgaard, et al., CBS, Technical University of
            Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
            SplicePredictor (Volker Brendel, Stanford University,
            http://gremlin1.zool.iastate.edu/cgi-bin/ap.cgi).

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Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MPA22 and the 3' clone is T31G3.

FEATURES             Location/Qualifiers
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     /chromosome="5"
     /clone="K12B20"
     /clone_lib="Mitsui TAC"
     /ecotype="Columbia"
     /notes="CDS is reported in Acc# AB025630
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     /number=1
     /evidence=not experimental
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     /evidence=not experimental
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     ASTGVLTARDNDNFALDALVATQKPLTSCSDTKDAHMLLNDKCLHRHC
     FSCVQKQVKLRSGIVPPCLDGCKSELTLSCSMVLTPKLIEMMKRKEEDLIPDA
     EKYCYPRSCMLMSKTELSAEQSNVRAICSELCFICDCKVPWHSLSADYKRI
     HSRLLVNDMLKVLANDQMRQCSECKHMLTEGCGNHITCRGVEFCYRCGKWKY
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     KSGDLVNAKLFDEMFKRDIISYTSIMIDGYAKGDMVSARDLFEARGVDVRAWALI
     LGYAQGNPNEAFKVFSECAKNVKPDEFIMVGLMSACQSQMGCFELCEKVDVSYLQRM
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     LFEKWDGIVPDEVAFTVLKVGQSLVEEGLRYFELMKKYSILASPDHYSCIVN
     LLSRTGKLKEAYELIKSMPEAHASAGSLGCSLHGNTKEIAEVAWHLFELEPQSA
     GSVLLSNLYAALDRWTDVAHLRDKNENGITKICGRSWISR"
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     EDSLQCVTFAYKEFGYGTQLQDSSEVSEVSLCKHLALAKKETTNSKASPISLP
     ELKEEKRIDIDRSQKTS"
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     gene_id:K12B20.5"

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complement (join (14277..14429,14527..14686,14767..14858,
14935..15138,15221..15415,15495..15543,15646..15749,
15838..15877,16286..16359))
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/evidence=not_experimental
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/db_xref="GI:9757970"
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IGADKSGRDVVDVSHYKACLVAGINISGINGEVMGOWEFOVGPAGVISADEIHWAR
YILRITELAGVVVSFDPKPIPGDMNGAGACHVSTKSMREEGVEIILKALDKLGR
HKEHIAAYEGENRRLRGHETADINTFLNGVANRGASIRVGRDTEKGGKGYFEDRRP
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CDS

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LHCDVCNFSICRACMNPPVGVESPTTHEQLHLVPRRIHFTCNACGLGEGSPIF
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KCLSFARHACATREDVWMEVELEGTEPEDEIGPEVIDDNTIKHSHDHLRLNNDG
DQILHENIVCEACALQILSEPPFYSCQCNFKLQKCAHPRKHVYRNLNPLFTLLTS
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KVNSEWYFNCDCGTLTHISCVGDFSYIKHGSMLNTRKVVSNISICRPFPCVCSR
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32169..32438,32552..32813,32936..33249)
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CDS

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DVIDCMRLVRDQVLTFRFAVSLRSPNDPENSIDLLEILLPLENVEVAKTV
LSLPPNATQAIIDCTLDVNESVRKAYSVLANKVPLOSILKRLTILORGLADRA
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KSIQOYLISADGETNDCSPASIQLMPEALYWRILICRKHOSQAQSGDAATM
GAEAAVAAASANDLLRLPATVSDVLDLVAHIEAGEPRYCFYENISCFCLGD
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VIGDINLGDDKDMAEAVSKLAKVHAAPGEYEEVILVVVEVARPCRERTADFLQNM
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LLGKIFNLFPASFPYFVGLKILIALYFSEESKEQLRPFQCLSVFHEHYASLSKHKGYV
SKAPFVLVRMWPMDIGNTSSSVYVNRKRRAVOVSRFLOMMQTPILYKKEITGEPE
PSONVTKLKLKLLSLADSVRSEKDLLEKVPVLQHLKSLDACPSELTOQDANSIF
EILGSYNLEITETTTPQTPAPCSTKPARRRARTBEETSSDEEVAVPPSPAPNTL
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/evidence=not_experimental

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CDS

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Query Match 5.0%; Score 127.2; DB 8; Length 78874;
Best Local Similarity 66.3%; Pred. No. 7.2e-15; Indels 3; Gaps 1;
Matches 199; Conservative 0; Mismatches 98;
Qy 103 GGTTCGGGATTGACGACGAGTACACCCCTTCTCCAGAGGACACCAAGTGGCTCTCGGTT 162
Db 15309 GGTATGGTATTGACAGAAATACACTTTACTCCAGAAAGATGTGAAGTGGCTGTGGTT 15250
Qy 163 GGCCGCTGGGGCTTACCCCTGCTCAGGTAGATTAGATGATCT---GGTGCCTCCA 219
Db 15249 GGCCTATTGGTGGTTATCCCGGCCCTCAGGTGAAGAAGATGATATAATCGGTTTTGT 15190
Qy 220 GGCTCCAGCCATATCGATGGCTTTGATCAGCTGACGGAATGATCTCGCAGGACCTTAC 279
Db 15189 ATCTTTTCGGTGTGGTTATCTTAAATTTTGGCGAAATATGATTTCGAGGACCGTAC 15130
Qy 280 TACTCGCGCGTCGAGCGGACAACTCTTACCGGCGGACATCGTGGACCGCAGCTACAAAG 339
Db 15129 TATTGGGTATTGGAGCAGACAAATCTTTTGCAGAGATGTTGTTGATCTTCACTACAAG 15070
Qy 340 GCCTGCTCTTACGCGGCGATCGATCATGTCGATCAACGCGGAGGATCATGCCGGGGCAG 399
Db 15069 GCCTGCTTATACGCTGGGATCAACATTAGTGGCATCAATGGAGAAGTCAATGCCGGGTCAG 15010

RESULT 3
AC082645/c AC082645 143681 bp DNA linear PLN 14-MAR-2001
LOCUS Oryza sativa chromosome 3 BAC OSJNB0033N16 genomic sequence,
DEFINITION complete sequence.
ACCESSION AC082645
VERSION AC082645.13 GI:13249436
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE 1 (bases 1 to 143681)
AUTHORS Buell, C.R., Yuan, Q., Ouyang, S., Moffat, K.S., Hill, J.N., Burr, P.C.,
Hsiao, J., Zismann, V., Pai, G., Bowman, C.L., Fujii, C.Y.,
VanAken, S.E., Bowman, C.L., Craven, B., Utterback, T.R., Khalak, H.,
Feldblum, T.V., Quackenbush, J., White, O., Salzberg, S.L. and
Fraser, C.M.
REFERENCE 2 (bases 1 to 143681)
AUTHORS Buell, R.
JOURNAL Direct Submission
REFERENCE 3 (bases 1 to 143681)
AUTHORS Buell, R.
JOURNAL Submitted (29-SEP-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 4 (bases 1 to 143681)
AUTHORS Buell, R.
JOURNAL Submitted (08-MAR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 5 (bases 1 to 143681)
AUTHORS Buell, R.
JOURNAL Submitted (08-MAR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA

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repeat_region complement(26630..26686)
/rpt_family="AT rich"
gene /gene="OSJNBb0033N16.11"
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GB:CAA65543 GI:1237029 (Bos primigenius)"
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VKDRFLRFEFTTQEVOLAPIRRPVSGVSLNOSPVTLSYPTENAVLICSDVDGSGYE
LYIVPKDSAGRADYLDQAKGAGSAVFVAENRFAVLEKSNQVLRNKLKNEIVKSP
LPATDAIYAGTSGLLCAEDRVTFIDLQORLLIGELQAFSVKTVVWSSDMESVALL

Query Match 4.8%; Score 123; DB 8; Length 143681;
Best Local Similarity 63.8%; Pred. No. 5.6e-14;
Matches 220; Conservative 0; Mismatches 120; Indels 5; Gaps 2;

QY 253 ACGGAATGATCTCGCAGGACCTTACTCTGCGCGGTGCGAGCGGACAAATCTCTACGGG 312
DB 123696 ACGAAATGGTGTGATAGGTCGCTACTGTGCGCGGCGGAGCGGACAAATCTCTACGGG 123637
QY 313 CGGACATCTGCGGACGCTACAAAGCGCTCTAGCGCGGATCGACATCAGTGGC 372
DB 123636 CGCGACATCTGTGATGCCACTACAAAGCGCTCTGTGCGGATCAACATCAGCGG 123577
QY 373 ATCAACGGGAGGTGATCGCGGCGAGGTACAGCGTCTGTCTAGTACCTTGTCTTTA 432
DB 123576 ATCAACGGAGATCATCGCGGCGAGGTAGAACATTTCTGNAATCTGCACACCT--- 123520
QY 433 ACTGCACACTGACTCTGCACACTGCACAGCTAGTAGTATGCTGCTATCTCTGTCGACCC 492
DB 123519 -CGCGTTTCTGTGCCATTTTTTTCGCGACACTTTGTCTCATGAGCTGATCGCTTGTAT 123461
QY 493 AGCGTTGTCGCGGACGTGGAGTTCCAGGTGCGGCGCTGCGTGGCGGTCTCGCGCGGC 552
DB 123460 GTGCGATTTGTGACAGTGGAGTTCAGATTGCGCCCTGTGTTGGCGTCTCCGCGAGG 123401
QY 553 GA-CAGCTTGGTGGGCTCGCTACATTTCTTGAGGAAACGGTAGA 596
DB 123400 GATCATGCTGGTGGCAGCTACATTTCTTGAGGTAGACTGAAA 123356

RESULT 4
LOCUS ZMG512 1369 bp mRNA linear PLN 09-DEC-1993
DEFINITION Z.mays mRNA gel-2 for glutamine synthetase.
ACCESSION X65927
VERSION X65927.1 GI:434325
KEYWORDS glutamine synthetase.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1369)
AUTHORS Li.M.G., Villemur,R., Hussey,P.J., Silflow,C.D., Gantt,J.S. and Snustad,D.P.
TITLE Differential expression of six glutamine synthetase genes in Zea mays
JOURNAL Plant Mol. Biol. 23 (2), 401-407 (1993)
MEDLINE 9403318
PUBMED 8106013

REFERENCE 2 (bases 1 to 1369)
AUTHORS Snustad,P.D.
TITLE Direct Submission
JOURNAL Submitted (28-APR-1992) P.D. Snustad, University of Minnesota, Dept of Genetics & Cell Biology, College of Biological Sciences, 250 Biosciences Center, 1445 Gortner Ave/St Paul MN 55108-1095, USA
COMMENT See also X65926-31.
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/db_xref="taxon:4577"
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/clone_lib="lambda gt10; Gantt"
/dev_stage="seedling"
1..1369
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103..1209
/gene="gs1-2"
/codon_start=1
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/protein_id="CAA46720.1"
/db_xref="GI:434326"
/db_xref="GOA:P38560"
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DDPSKLKPNWFDGSGTCAQPGDDSEVILCPRAIFRDPFRKQNLVIMCDDCFEPNPEPI
PSNRKGAARIPSHPDVKAEPFGEIYLLQKDTKPLGWPLAYVPGQPGPYCAA
GADSKYGRDVIDCAKACIAGIDISINGEIMFQWFEVAPVAGAGDQLWVARY
ILERITIAVVSFDPKPIPDGWNAGAHNTYTSKMSRSDGGEVIKKAIGKGLRH
REHTAAYDGNRPLTGRHETADINTFVWGVNKGASVRVGRDTEKEGKGVFEDRRPA
SNMDPVVYVTCILIAETITLWLEPSSHSGDGKGAAP"

ORIGIN
Query Match 4.8%; Score 122.6; DB 8; Length 1369;
Best Local Similarity 87.6%; Pred. No. 3.2e-14;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 247 CAGCTGACGGAATGATCTCTGCGAGGACCTTACTCTGCGCGGTGCGAGCGGACAAATGCC 306
DB 538 CCGTGGGTGATACCTGCGCCCTCAGGACCTTACTCTGCGCGGTGCGAGCGGACAAATGCC 597
QY 307 TACGCGCGGACATCTGCGACGCGACACAAAGGCTGCTCTAGCGCGGATCGACATC 366
DB 598 TACGCGCGGACATCTGCGACGCGACAAAGGCTGCTCTAGCGCGGATCGACATC 657
QY 367 AGTGGCATCAACGGGAGGTGATCGCGGGCAG 399
DB 658 AGTGGCATCAACGGGAGGTGATCGCGGGCAG 690

333-399

AB019230 74968 bp DNA linear PLN 14-FEB-2004
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBBS.
AB019230 BA000034
AB019230.1 GI:3869069
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asanizu,E. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 3. I.
Sequence features of the regions of 4,504,864 bp covered by sixty
P1 and TAC clones
DNA Res. 7 (2), 131-135 (2000)
MEDLINE 20277480
PUBMED 10819329
REFERENCE 2 (bases 1 to 74968)

AUTHORS Sato, S., Nakamura, Y., Kaneko, T., Kato, T., Asanizu, E. and Tabata, S.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan [E-mail: ynakamu@kazusa.or.jp, Tel: 81-438-52-3935, Fax: 81-438-52-3934]
 COMMENT Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/aggd_graph.cgi?c=MEB5
 'product' with similarity to proteins in the databases are described in 'product' or 'note' Qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: GraIL (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/GraIL-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>), SplicePredictor (Volker Brendel, Stanford University, <http://gremlini.zoology.ualb.ca/edu/cgi-bin/ep.cgi>).
 Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).
 This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MIG5 and the 3' clone is MBG14.
 Location/Qualifiers
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 /mol_type="genomic DNA"
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 /note="unnamed protein product; gb|AAP02142.1
 gene_id:MEB5.2
 similar to unknown protein"
 /codon_start=1
 /evidence=not experimental
 /protein_id="BAB02703.1"
 /db_xref="GI:9294484"
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 join(4833, .5114, 5267, .5530, 5646, .5816, 6010, .6122, 6214, .6397, 6484, .6593, 6687, .6843)
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 /codon_start=1
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 /translation="MASMSPALNRFSGLSKSTTSLADFPSSRRSLPPTRVGLKISS AAESPDLSVTYVNLGMPNPFVIGSGPPGNTYTMKRAFDEGMAVIAKTVSLDASKV INVTYARLRTSGNSGAKTDVIGWONIELISDRPLETLMKEAFGLKEYVDRILIAS VMKEYNTAAWEELIDRVEQGVDALEINFSCPHGMPERRMGAAVGOCCALLDPCVGIW GADKAIGRDIYDAHYKACLYAGIGISGINGEVMPPQMGVEGQVPGDQVYVAR YLLERITEISGVISFPDPKVPDGMWAGAHACNYSTKTRNDGGLGLEYIKKAIKQLK HKEHIAAYGGBNRRLLTGKHETADINTFSMGVANRGASVRVGRDKEGKGYPEDRR ASNMDPVVVTSMIAETILG"
 join(14242, .12688, 12793, .12861, 12959, .13054, 13143, .13267, 13534, .13729, 13834, .14009, 14094, .14223, 14304, .14464, 14549, .14645)
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 /db_xref="GI:9294487"
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 join(16646, .17996, 18392, .18984)
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 /codon_start=1
 /evidence=not experimental
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 /protein_id="BAB02707.1"
 /db_xref="GI:9294488"
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 complement(join(20408, .20494, 20905, .21059, 21182, .21278, 21361, .21417, 21496, .21547, 21653, .21741, 21948, .22033, 22339, .22543, 22660, .22752, 22834, .22974, 23048, .23140, 23292, .23535, 23680, .23852, 23947, .25299, 25378, .25560, 25666, .25730, 25899, .26001, 26041, .26763, 26845, .27042))
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Qy 359 TCGACATCAGTGGCATCAACGGGAGGTTCATCGCGGGCAGGTACAGCGTCTGCTCTAG 418
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 Qy 4733 TCAACATCAGTGGATCAACGGCAGGTTCATCGCGAGCAGGTGAACACTACTCTCAAC 4792
 Db |||||
 Qy 419 CTACCTTGTCTTTAACTGACACTGCATCTGACACTGCACAGCT----- 464
 Db |||||
 Qy 4793 CTTGCCATTTCTATCGTCTCTGAATAGTGGAGTACATTTCTGACCATGCTAAATATCGTA 4852
 Db |||||
 Qy 465 --AGTAGTATCTGCTATCTCTGTCGACCCAGGCTTGTTCGTGACAGTGGAGTTCAG 522
 Db |||||
 Qy 4853 TCAGATCTATAAATGGTAATGTTATTAACATTTGTGATCGGTTTTTTCAGTGGAGTCCAA 4912
 Db |||||
 Qy 523 GTGCGCCCTGCGCTCGCGTCTCGCGCGCA-CAGCTTGGTGGTCTGCTACATCTT 581
 Db |||||
 Qy 4913 GTTGGCCGCTGTCGCGCATTTCTGCGCGTATCAGGTGGTGGTCTGCTACATCTT 4972
 Db |||||
 Qy 582 GAGGAA 587
 Db |||||
 Qy 4973 GAGGTA 4978
 Db |||||

RESULT 7
 AP004880/c
 LOCUS
 DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
 PAC clone: P0487D09.
 ACCESSION AP004880
 VERSION AP004880.3 GI:46390424
 SOURCE Oryza sativa (japonica cultivar-group)
 KEYWORDS Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 1 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC
 clone, P0487D09
 Published Only in Database (2002)
 2 (bases 1 to 161531)
 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Direct Submission
 Submitted (20-MAR-2002) Takui Sasaki, National Institute of
 Agrobiological Sciences, Rice Genome Research Program; Kamondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail: tsasakienia@affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
 Tel: 81-299-38-7441, Fax: 81-299-38-7468)
 On Apr 14, 2004 this sequence version replaced gi:33235578.
 Genes were predicted from the integrated results of the following:
 GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
 (http://www.softberry.com/), GeneMark.hmm
 (http://opal.biology.gatech.edu/GeneMark/), GlimmerM
 (http://www.tigr.org/tdb/glimmer/glmr form.html), RicheHM
 (http://rgp.dna.affrc.go.jp/RicheHM/), SplicePredictor
 (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
 (http://globin.cse.psu.edu/html/docs/sim4.html), gap2
 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The
 genomic sequence was searched against NCBI NonRedundant Protein
 database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
 sequence database at RGP or DBJ. Protein homologues of the coding
 regions were searched against NCBI NonRedundant Protein database
 with BLASTP. ESTs represent the identified cDNA sequences using
 BLASTN with the corresponding DBJ accession no. and RGP clone ID.
 Full-length cDNAs represent the identified cDNA sequences using
 BLASTN with the corresponding DBJ accession no.
 A gene with identity or significant homology to a protein is
 classified based on the protein name to indicate the homology level
 such as same name, 'putative-' and '-like protein'. A gene without
 significant homology to any protein but with full-length cDNA or
 EST homology (covering almost the entire length of partial
 sequence) is classified as an 'unknown' protein. A gene predicted
 by two or more gene prediction programs is classified as a
 'hypothetical' protein according to IRGSP standard. A gene

predicted by a single gene prediction program is also classified as
 a probable 'hypothetical' protein and is included as a
 miscellaneous feature of the sequence.
 The orientation of the sequence is from SP6 to T7 of the PAC clone.
 This sequence of P0487D09 clone has an overlap with P0643A10 (DBJ:
 AP005319) clone at 5' end and with P0684F11 (DBJ: AP005112) at 3'
 end. Detailed information on overlap and assembly quality together
 with annotation of this entry is available at
 http://rgp.dna.affrc.go.jp/GenomeSeq.html.

FEATURES
source

1. 161531
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 12806..13234)
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 12806..13234)
 /note="supported by full-length cDNA(s) : AK070347"
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 12806..12956)
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 /notes="contains EST(s) : D46622(S11405), AU088653(S11405)
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 PAVAAALLFFPMFFGSHTPAAAYGEASGDAGVTALQKHAAPFKDGGDGVLSLE
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 YDGEFRFAEKPEEIPAKHAKTPVDALTSDEIDELQANRKPQDGTGWAASSEWKIL
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	AB008270	50641 bp	DNA	linear	PLN 14-FEB-2004
LOCUS	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTG13.				
DEFINITION	AB008270 BA000015				
ACCESSION	AB008270.1 GI:2618604				
VERSION					
KEYWORDS					
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids;				
REFERENCE	1 Nakamura,Y., Sato,S., Kaneko,T., Kotani,H., Asamizu,E., Miyajima,N. and Tabata,S.				
AUTHORS	Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned p1 clones				
TITLE	DNA Res. 4 (6), 401-414 (1997)				
JOURNAL	951997				
MEDLINE	2 (bases 1 to 50641)				
PUBMED	Nakamura,Y.				
REFERENCE	Direct Submission				
AUTHORS	Submitted (24-OCT-1997) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana,				
TITLE	Kisarazu, Chiba 292-0812, Japan [E-mail:yinakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934]				
JOURNAL	Address for correspondence: kaos@kazusa.or.jp				
COMMENT	For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MTG13 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3//), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlin.zool.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MQK4 and the 3' clone is F5E19.				
FEATURES	Location/Qualifiers				
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CDS	8405..8453,8546..8649,8766..8805,9161..9234))				
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	/evidence=not experimental				
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	/db_xref="GI:10176966"				
	/translation="MSSLAADLNLDLSDTQIIAEYIWIIGSGGLDMRSKARTLPGPVTPDQLPNWYDGSQTGAQDESEVIYPOAIFKPPFRGNLLVMCDATYTAGPIPTNKRAAKIPEDPSVAEEETWIEOEYITLLOKIKWPVPVGFGPQGPGPYTCGVADKAQRDIIVDSHYKACLAVINGSTNGEVMPGWOFVGTGIAAADOVWARYLIERITELAGVLISDPKPIPDWGNGAGAHNTYSTKMREDGGYEVIKAIKLGLIRKHETAAEGENRERLTGHETADINTFLMGVANRGASIRVGRTEOAGKGFYEDRRPASNMDDPYTVTSMAESTILWKRP"				
	complement(join(10396..10528,10717..10847,10895..11019,11247..11470,11565..11683,11773..11990,12108..12183))				
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	/codon_start=1				
	/evidence=not experimental				
	/product="receptor-like protein kinase"				
	/protein_id="BAB10186.1"				
	/db_xref="GI:10176968"				
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	join(23002..23134,23712..23841,24205..24925)				
CDS	23002..23134,23712..23841,24205..24925)				
	/note="gb AAD53095.1"				
	gene_id:MTG13.4"				
	/codon_start=1				
	/evidence=not experimental				
	/product="transcription factor"				
	/protein_id="BAB10187.1"				
	/db_xref="GI:10176969"				
	/translation="MGKPCCDKVGLKKGKWPTEEKDLINFLTNHGHCWRALPKULS GLLKCGSCRLRWNYLRPLDKLGLLSEYEQKVINHAQIGNRWKIASHLPERTDN ELKHNWNTIKKLRKMGIDPLTHKPLSEQAQOQRKSLVPHDDKNPKQDOQTK DEQHOLEAQALEXNNTSVSGDFCIDEPDLLNPHELIDISSHHHSNDNNVINT SKFTSPSSSSSTSCISVVGPGEFSKFFDEMELIDLKWLSDSDSIGDDISKDGKEN NSTVDTMLWDINDLSSLDMPNEHDGFTGNGCSRMVLDQDSWTFDILL"				
	complement(join(29779..30054,30150..30303,30375..30466,30545..30649,30722..30847,30929..30977,31074..31819,31908..31941,32328..32423,32505..32656))				
CDS	29779..30054,30150..30303,30375..30466,30545..30649,30722..30847,30929..30977,31074..31819,31908..31941,32328..32423,32505..32656)				
	/note="unnamed protein product; gene_id:MTG13.5"				
	unknown protein"				
	/codon_start=1				
	/evidence=not experimental				

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Db	7660	AGAGACATCGTGTATTCTCATTACAAAGCTTGTCTTTACGCCGGAATCAATGTCTAGTGG	7601
Qy	373	ATCAACGGGAGGTATCGCGGGGAGGTACAGCGTCTGTCTAGCTACCTTGTCTTTA	432
Db	7600	ACTAACGGCGAAGTTATGCGCTGGCCAGGTTTACTTTTACGCCCTTCTCTATATATTTCTCTG	7541
Qy	433	ACTGCACACTGCACCTCTGCACACTGCACACTAGTAGTAGTCTATCTCTGCTGACCC	492
Db	7540	ATTTCAATATC-----AGAACAAAGAAACCAATCTTTGAAACTG	7503
Qy	493	AGGCTTCTTCTGTGGACAGTGGGAGTTCAGGTGCGCCCTGCGCGCGGTCTCGGCCGCG	552
Db	7502	AGCTTGTGTGGTTCAGTGGGAGTTCCAAGTCGGTCCACCGTTGGAATCGTCTGCCGC	7443
Qy	553	GA-CAGCTTGGGTGGCTCGCTACATCTTTGAGGAAACCGTAGACCTGCCCTGCGG	610
Db	7442	GATCAGGTCTGGGTGCTCGTTCATCTTTGAGGTAATATATAAACCAACTCATGGC	7384
RESULT 11			
AY491969			
LOCUS	Triticum aestivum glutamine synthetase isoform Gsr2 (GS) gene, complete cds.	1341 bp	linear
DEFINITION	Triticum aestivum glutamine synthetase isoform Gsr2 (GS) gene, complete cds.		PLN 28-DEC-2003
ACCESSION	AY491969		
VERSION	AY491969.1	GI:40317417	
KEYWORDS			
SOURCE	Triticum aestivum (bread wheat)		
ORGANISM	Triticum aestivum		
REFERENCE	1 (bases 1 to 1341)		
AUTHORS	Dionisio,G., Jahn,T.P. and Schjoerring,J.K.		
CONSTRM	Plant Biotechnology Consortium (DK)		
TITLE	Cloning of wheat glutamine synthetase isoforms by functional complementation and RACE PCR		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1341)		
AUTHORS	Dionisio,G., Jahn,T.P. and Schjoerring,J.K.		
CONSTRM	Plant Biotechnology Consortium (DK)		
TITLE	Direct Submision		
JOURNAL	Submitted (01-DEC-2003) Plant Nutrition, The Royal Veterinary and Agricultural University (KVL), Thorvaldsensvej 40, Frederiksberg C, Copenhagen DK-1871, Denmark		
FEATURES	Location/Qualifiers		
source	1..1341		
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	/tissue_type="root"		
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	/protein_id="AA84348.1"		
	/db_xref="GI:40317418"		
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tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).
Simple repeats are identified by repeatmasker (Arian Smit,
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

FEATURES

Location/Qualifiers

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/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Columbia"

/db_xref="taxon:3702"

/chromosome="1"

/clone="F15E12"

109..852

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/codon_start=1

/product="hypothetical protein"

/protein_id="AAG51295.1"

/db_xref="GI:12322601"

/translation="NRVYSSKEPRVPVEIRGAMRCLHVIIFLIEASLNAVHILSP

ILISCLSEQVSDSLKILMLNVAFEITIQEWTYDLREFFISKAESFVKVVS

VFKLSMPDLDEEFLIPMENLLPAIRKLGDNEDSSQWGLAPVGGFCAVHLLET

TRVDLVLENLMEKSVKRGMEGLFLGKALRDVEIAVVEQLMWTCTTFRFVLGLIQR

VEAIVTEETTKNVLQRIKIVVKKMLEYA"

complement (1259..1616)

/note="F15E12.21"

/gene="pseudogene, hypothetical protein (fragment)"

/pseudo

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/note="contains Pfam profile: PF01397: Terpene synthase

family"

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4596..4737,4923..5171,5265..5558)

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4596..4737,4923..5171,5265..5558)

/gene="F15E12.3"

/codon_start=1

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SHLESIAACCTCPPLSVHIONVLSVQHNMEILVPEYIPFYEQEKDEHLLKF

AKLSFLQLQVTDQLKIVTWYKELEPASKLPYFRDNIWVNTFYVLAVITYPHQSY

ERIMLTQVFTCLAILDDTFDRVASLPEPAISLANSLEWAPNDAMDQPDYLVKLVNFI

LKTFEYFOKELEPEGRSVTVKATIEEFKTVTKGNFDLAKWAHVAHVPSPEYMEVGE

EISVCSLGIAPMCMEQKATKDEYWLKSRPKFIQTLCARCLKNIDITGPFDDMSRGY

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8710..9213

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/protein_id="AAG51313.1"

/db_xref="GI:12322619"

/translation="MALIGLEAFIAFVCFILFYFYLLIKPKYSYLIIKISGSLWNWP

VLGMPGLMPRIYDFSVLLENSNLTFFHKGFWFAGIDILATADSVNTHIYYRG

PELRIFGPGDGIINSDELWRLKKATQVIFNHQYKFSTSTRSKLGLGLVPLF

NDHENLK"

complement (9381..12242)

/gene="F15E12.8"

/note="contains Pfam profile: PF00097: Zinc finger, C3HC4

type (RING finger)"

mRNA

CDS

complement (join(<9381..9551,9647..9861,9942..10071,
10159..10261,10347..10411,10502..10601,10742..10867,
10963..11498,11820..>12242))
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complement (join(9381..9551,9647..9861,9942..10071,
10159..10261,10347..10411,10502..10601,10742..10867,
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/db_xref="GI:12322600"

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GKLTCLCRSKIPRHAKNPRINLALYSAIRLANVTKCSGEATKAVHHIIRNODRPD

KAFTTERAVTKGANAAGSKFVTIPRDHFGPIPAANDVTRNGVGLVESWEDROECR

QMGVHFPHVAGIAGAAAGSVALSGYDDEHDEHGFYTGSGGRDLSGNKYNKI

QSSDQAFKNMNEALRLSCMGYPVVRWSKEKRSAYAPAEGRVTDGYRIEKWSNV

GVQGLHKMCRYLFRCDNEPAPMTSDEHGRPRPLDPPELENATDLPVKRESWGF

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VTTCAHNFCACLEAKFAGITQLDRSNGVRKLRAKNIMTCCCTTDLSEFLQNPQ

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/note="contains PF00097: Zinc finger, C3HC4 type (RING

finger)"

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join(15095..15517,16057..16342,16418..16592,16688..16813,

16954..17053,17144..17208,17294..17396,17484..17613,

17694..17908,18004..18177)

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/protein_id="AAG51305.1"

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GKLTCLCRSKIPRHAKNPRINLALYSAIRLANVTKCSGEATKAVHHIIRNODRPD

KAFTTERAVTKGANAAGSLVSGSWEDROECRQMGVHFPHVAGIAGAAAGSVAL

SGYDDDDHGEWFLYTGSGRDLSGNKNVNIQSSDQAFKNMNEALRLSCMGYPVVR

VWRSEKRSAYAPAEGRVTDGYRIEKWSNGVQGLHKMCRYLFRCDNEPAPMTS

DEHGRPRPLDPPELENATDLPVKRESWGFDEAGRWKWKSPVSRMALDTER

KKKRAKGNAMKARLLKEFCQICRKLVSLLPVTTCAHNFCACLEAKFAGITQLR

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NISSEEESESESEPTKKIKMDKNSVGGTSLSA"

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/gene="F15E12.9"

complement (<19746..>20693)

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complement (19746..20693)

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/codon_start=1

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/db_xref="GI:12322604"

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AESEFKAQSVFSLSNPLDGEFLIPMDNLLPAILKRLGNKEEESQWGLAPVGG

FCFAVHLLETTRVDLVLENLMEKSVKRGMEGLFLGKALREVEIAVVEQLMWTCTTE

FRFVILGIRIDAIIVTEETANKVLQRIKIVVKKMLEYV"

complement (21755..23081)

/gene="F15E12.10"

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22473..22621,22749..22870,23069..>23081))

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complement (join(21755..21846,21954..22110,22202..22349,

22473..22621,22749..22870,23069..23081))

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Best Local Similarity	62.2%; Pred. No. 8.2e-11;
Matches 194; Conservative	0; Mismatches 103; Indels 15; Gaps 1;
QY 102 AGGTTGGGATGAGCAGAGTACACCTTCTCCAGAGGACACAAAGTGGCCTCTCGGT 161	
D 82135 AGGTATGAAATCGAACAGAAATACACTTGTGTGCAAGAGGATGTGAATGCGCCTCTTGGGA 82076	
QY 162 TGGCGCTGGGGGCTACCTCGCCCTCAGGTAGATAGATGATCGTGGCTCCAGG 221	
D 82075 TGGCCCATGTGTGGCTCCCTCGGCCCTCAGTACATTCCTGCGGAGTATTTTCGT 82016	
QY 222 CTCAGCCCATATCGATGGCTTTGATCAGCTGACGGAATG-----ATCGTG 266	
D 82015 TTGTTACTGCTCTTTTCGATTCTCCGTTCTTGCTTCTGAATTATCTTGCACCTTT 81956	
QY 267 GCAGGACCTTACTCTGCGCGCTGGAGCGGACAAAGTCTCTACGGCGGGACATCGTGGGA 326	
D 81955 GCAGGACCTACTACTCTGAGTATTTGGAGCTGACAAATCTTTTGAAGAGACATTGTTGA 81896	
QY 327 CGGCACCTACAGCGCTGCTTACGCCGCGCATCGACATCAGTCGATCAACGGGGAGGT 386	
D 81895 TGCTACTACAAAGCCTCTTTGTATGCTGGAATCAACATCAGTGGGATCAATGAGAAGT 81836	
QY 387 CATGCCGGGGCA 398	
D 81835 CATGCCGGGACA 81824	
RESULT 14	
LOCUS	AY491970
DEFINITION	Triticum aestivum glutamine synthetase isoform GSe1 (GS) gene, complete cds.
ACCESSION	AY491970
VERSION	AY491970.1 GI:40317419
KEYWORDS	Triticum aestivum (bread wheat)
SOURCE	Triticum aestivum
ORGANISM	Triticum aestivum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
AUTHORS	Dionisio,G., Jahn,T.P. and Schjoerring,J.K.
CONSRM	Plant Biotechnology Consortium (DK)
TITLE	Cloning of wheat glutamine synthetase isoforms by functional complementation and RACE PCR
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1299)
AUTHORS	Dionisio,G., Jahn,T.P. and Schjoerring,J.K.
CONSRM	Plant Biotechnology Consortium (DK)
TITLE	Direct Submission
JOURNAL	Submitted (01-DEC-2003) Plant Nutrition, The Royal Veterinary and Agricultural University (KVL), Thorvaldsensvej 40, Frederiksberg C, Copenhagen DK-1871, Denmark
FEATURES	Location/Qualifiers
source	1. .1299
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	/mol_type="genomic DNA"
	/db_xref="taxon:4565"
	/tissue type="root"
gene	<82. .>1170
	/gene="GS"
mRNA	<82. .>1170
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CDS	/product="glutamine synthetase isoform GSe1"
	82. .1170
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/note="GS subunit"	
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AGAEKSYRDIIVDAHYKACLYAGINIGINAEVMPQWQFQVQSPVSGISAGDELWAAR	
YLLERITETAGVIVVDFPKPIPGEMWAGAHNTYSTKMSRSEGGYEVIKAIQKLEAR	
HMEHIIAAYGSEGNRRLLTGRHETADINTFVMGVANRGASVRVGRDTEKEGKGFEDRRP	
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ORIGIN	
Query Match	4.1%; Score 104.8; DB 8; Length 1299;
Best Local Similarity	87.1%; Pred. No. 1.3e-10;
Matches 115; Conservative	0; Mismatches 17; Indels 0; Gaps 0;
QY 268 CAGGGACCTTACTACTCGCGCTCGGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 327	
D 541 CAGGGACCTTACTACTCGCGCGGTGCGGAGAAATCTTACGGCGCGACATCGTCGAC 600	
QY 328 GCGCACTACAAGCGCTGCTCTTACGGCGGCATCGACATCAGTCGATCAACGGGGAGTGC 387	
D 601 GCGCACTACAAGCGCTGCTCTTACGGCGGCATCAACATCGCGGCATCAATGCAGAAATGC 660	
QY 388 ATGCCGGGGCAG 399	
D 661 ATGCCAGGACAG 672	
RESULT 15	
LOCUS	ZMG514
DEFINITION	Z.mays mRNA gsl-4 for glutamine synthetase.
ACCESSION	X65929
VERSION	X65929.1 GI:434329
KEYWORDS	glutamine synthetase.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 1490)
	Li,M.G., Villemur,R., Husey,P.J., Silflow,C.D., Gantt,J.S. and Snustad,D.P.
TITLE	Differential expression of six glutamine synthetase genes in Zea mays
JOURNAL	Plant Mol. Biol. 23 (2), 401-407 (1993)
MEDLINE	94033318
PUBMED	8106013
REFERENCE	2 (bases 1 to 1490)
AUTHORS	Snustad,P.D.
TITLE	Direct Submission
JOURNAL	Submitted (28-APR-1992) P.D. Snustad, University of Minnesota, Dept of Genetics & Cell Biology, College of Biological Sciences, 250 BioSciences Center, 1445 Gortner Ave/St Paul MN 55108-1095, USA
COMMENT	See also X65926-31.
FEATURES	Location/Qualifiers
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	/clone="pGSL-4"
	/clone lib="lambda gt10; Gantt"
	/dev stage="seedling"
gene	1. .1490
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	85. .1152
CDS	/gene="gsl-4"
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	/product="glutamine synthetase"

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2005, 14:24:46 ; Search time 8062 Seconds
(without alignments)
12025.514 Million cell updates/sec

Title: US-09-989-739-18
Perfect score: 2547
Sequence: 1 ccattgctccgtacctcccc.....gctcgtcgctgctgctt 2547

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	587.6	23.1	951	9	CG115681 PUJGP86TD
2	562.2	22.1	797	8	CG343195 OGSAC35TV
3	561.2	22.0	796	9	CG014631 ZUAHC10TH
4	551.2	21.6	800	9	CG607969 OGUKR47TH
5	546.8	21.5	876	9	CG999928 ZMMBBB053
6	540.6	21.2	974	8	CG013698 FUEAAL6TD
7	538	21.1	681	9	CG937355 ZMMBBB022
8	502	19.7	860	9	CG363992 OGSAC35TV
9	501.8	19.7	802	9	CG221794 OGKWK20TV
10	485.2	18.3	627	9	CG891370 ZMMBBB037
11	460.6	18.1	888	9	CG213069 OG3CJ09TH
12	420.6	16.5	937	9	CG115678 PUJGP86TB
13	381	15.0	621	9	CG303139 OGVDX90TV
14	288.6	11.3	737	8	B2401579 OGABN93TC
15	283.4	11.1	344	9	CG865571 ZMMBBB033
16	270.4	10.6	734	8	B2401584 OGABN93TM
17	259	10.2	625	8	B2406372 OGABM94TM
18	254.2	10.0	647	8	B2365761 ie2h08.9
19	254.2	10.0	765	8	B2373733 ie12h08.9
20	254.2	10.0	796	8	B2810088 PUHAD25TD
21	239	9.4	510	9	CG727481 OGKAO19TH
22	220.6	8.7	887	9	CG213081 OG3CJ09TV
23	175.8	6.9	765	8	B2719724 FUDBB95TD
24	172.6	6.8	348	8	B2412338 OGACA09TC

ALIGNMENTS

RESULT 1
CG115681 CG115681 951 bp DNA linear GSS 20-AUG-2003
LOCUS PUJGP86TD ZM_0.6.1.0.KB Zea mays genomic clone ZMMBTa0663P04,
DEFINITION genomic survey sequence.
ACCESSION CG115681
VERSION CG115681.1 GI:33999118
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 951)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,U. and Bennettzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUJGP86TB
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
Location/Qualifiers
1. 951
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Best Local Similarity 86.5%; Pred. No. 4.4e-124;
Matches 758; Conservative 0; Mismatches 69; Indels 49; Gaps 8;
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Db 105 CCATGGTCCGTACCTTCCCTGCTGCACGAAATGAACCGACCTGTTGCGTACAGACATT 164


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Db 155 ATGGCGTGTGAGTGTGTTTCTGATGAGACGTTTCTTCTTCCCTGTGACTGGCAGA 96
Qy 715 GGAT-ACCGAGATCCCGCGGTGGTGTCTTCTCGACCCCAA--CCAAATTCGGTGACCA 771
Db 95 GGATCACCAGATCCCGCGGTGGTGTCTTCTCGACCCCAAGCCAATTCGGTGACCA 36
Qy 772 -TTGCTACCAACAATTTTGGGTTTGGATATGTGG 805
Db 35 TTTCGCTACCAACAATTTTCGGTTTGGATATGTGG 1

RESULT 3
CG014631/c
LOCUS
DEFINITION
ZUAH10TH ZM_3.0_4.0_KB Zea mays genomic clone ZMMBPa0068A19,
genomic survey sequence.
ACCESSION
CG014631
VERSION
CG014631.1 GI:33886796
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 796)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
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Location/Qualifiers
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Db 779 CCATGGTCCGTACCTTCCCTCGCTGACGAAATGAACCGACCTGTTCCGTACAGACATT 720
Qy 61 TCGTCGAAATGGTTCTTCTTACCGTGGACCTGTGTAAATCCAGGTTCCGGATGAGCAGG 120
Db 719 TCGTCGAAATGGTTCTTCTTACCGTGGACCTGTGTAAATCCAGGTTCCGGATGAGCAGG 660
Qy 121 AGTACACCTTCTCCAGAGGACCAAGTGGCTCTCGGTGGCGGTGGCGGCTACC 180
Db 659 AGTACACCTTCTCCAGAGGACCAAGTGGCTCTCGGTGGCGGTGGCGGCTACC 600
Qy 181 CTGGCCCTCAGTAGATTAGATGATCTCGCTGCCCTCCAGGCTCCAGGCATATCGATGCC 240
Db 599 CTGGCCCTCAGTAGATTAGATGATCTCGCTGCCCTCCAGGCTCCAGGCATATCGATGCC 540
Qy 241 TTGATCAGCTGACGGAATGATCTCGGAGGGAACCTTACTACTCGCGCGTCCGAGCGGAC 300
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Db 539 TTTGATCAGTCGCGGAATGATCTCGCAGGGAACCTTACTACTGCGCGTCCGAGCGGAC 480
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Db 479 AAGTCTTACGGCGGGGACATCGTGGACGCGCACTACAGGCTGCTCTTACGCGGCAATC 420
Qy 361 GACATCAGTGCATCAACGGGGAGGTATGTCGGGGGAGGTACAGCGTGTCTAGCT 420
Db 419 GACATCAGTGCATCAACGGGGAGGTATGTCGGGGGAGGTACAGCGTGTCTAGCT 368
Qy 421 ACCTTGTCTTTAACTGCACACTGCACACTGTGCACACTGACAGCTAGTAGTAGTCTAT 480
Db 367 -----CTGCACACTGCACAGCTAGTAGTAGTCTAT 335
Qy 481 CTCTGTGACCCAGCGCTTGTTCGTGGACAGTGGAGTTCCAGGTCGGCCCTGCGCTCGGC 540
Db 334 CTCTGTGACCCAGCGCTTGTTCGTGGACAGTGGAGTTCCAGGTCGGCTCTGCGCTCGGC 275
Qy 541 GTCTCGGCGGGCGA-CAGCTTTGGGTGGGCTCGCTACATTTTGAGGAAAAACGGTAGACCT 599
Db 274 GTCTCGGCGGGCGACAGCTCTGGGTGGCTCGCTACATTTTGAGGTAGACGGTAGACCA 215
Qy 600 GCGCCCTCGCGGCTGTGTTCGGTCTTCTTCG--CGAGACATGGCGTCTTGGCGAAC 657
Db 214 CTAGACCTGTCTGCGGCATGCGCGGTGTTCAGTTCTTCTTCTTCTTCTTCTTCTTCTT 155
Qy 658 TTTCGGGTGTGAGTGTGTTTGTGAGTGTGAGAGC--TGTCCTTTTCCCTGTGACTGGCAGA 714
Db 154 ATGCGGTGTGAGTGTGTTTGTGAGTGTGAGAGC--TGTCCTTTTCCCTGTGACTGGCAGA 95
Qy 715 GGAT-ACCGAGATCCCGCGGTGGTGTCTTCTTTCGACCCCAA--CCAAATTCGGTGACCA 771
Db 94 GGATCACCAGATCCCGCGGTGGTGTCTTCTTTCGACCCCAAAGCAATTCGGTGACCA 35
Qy 772 -TTGCTACCAACAATTTTGGGTTTGGATATGTG 804
Db 34 TTTCGCTACCAACAATTTTCGGTTTGGATATGTG 1
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LOCUS
DEFINITION
OGUKR47TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0463G22,
genomic survey sequence.
ACCESSION
CC607969
VERSION
CC607969.1 GI:31969390
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 800)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGUKR47TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
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Db 547 AGTTTCGCCCTTCACAAGTGGTTTCCCTCTCCAAGCGGCTTTTCCACTTTGTGAAATG 606
Qy 1447 ACAACTGCACCACTTGTCTATTATATATATATAATAAGGATAATATACTACAAAATATACA 1506
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Qy 1507 ATACATCCATTCGGATTTTATATTTTGGTATCAATTTTCCACAAGTTTGTATCGACTCGCC 1566
Db 664 ATACACCCGTTCCGATTTTATATTTTGGTTTCTACTTTTCCACAAATTTGGCGGACTCATC 723
Qy 1567 TTATTTTAAACTTGTACGAAAA---ATAAAATTAATACTACTATAATAATATATATCATG 1623
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Qy 1624 TGCTAAATAATATACAGTAATAATAATAATAATAATTTTTTTTGAATAAGACGAG 1683
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Db 841 TCGATTAAACCTGAACATAATA 864

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LOCUS FURAA16TD_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZM8Bta189C07,
DEFINITION genomic survey sequence.
ACCESSION CC013698
VERSION CC013698.1 GI:29397202
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Renick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
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Cot selected genomic DNA library"

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Query Match 21.2%; Score 540.6; DB 8; Length 974;
Best Local Similarity 86.9%; Pred. No. 2.8e-113;
Matches 668; Conservative 0; Mismatches 59; Indels 42; Gaps 5;

Qy 1 CCATGGTCGTACCTTCCCTCGCTGCAGGAAATGAACCGACCTGTGGGTACAGACATT 60
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Qy 121 AGTACACCTTCTCCAGAAGGACACCAAGTGGCCTCTCGTTGGCCGCTGGCGCGGTACC 180
Db 618 AGTACACCTTCTCCAGAAGGACACCAAGTGGCCTCTCGTTGGCCGCTGGCGCGGTACC 559
Qy 181 CTGGCCCTCAGTAGATTAGATGGATCTGCGTGCCTCCAGGCTCCAGCCATATCCATGCGC 240
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Qy 241 TTTGATCAGCTGACGGAATGATCTCGCAGGAGACCTTACTACTGCGCGCTCGGACGGAC 300
Db 498 TTTGATCAGCTGACGGAATGATCTCGCAGGAGACCTTACTACTGCGCGCTCGGACGGAC 439
Qy 301 AAGTCTACAGCGCGGAGCATCTGTGACCGCACTACAAGGCTGCTCTACGCCGCGATC 360
Db 438 AAGTCTACAGCGCGGAGCATCTGTGACCGCACTACAAGGCTGCTCTACGCCGCGATC 379
Qy 361 GACATCAGTGCATCAACGGGAGGTCTATCGCGGAGGTACAGCGTGTCTCTAGCT 420
Db 378 GACATCAGTGCATCAACGGGAGGTCTATCGCGGAGGTACAGCGTGTCTCTAGCT 327
Qy 421 ACCTTGTCTTTAACTGCACACTCTGCACACTCTGCACACTGACACTAGTAGTAGTGTCTAT 480
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Qy 481 CTCTGCTGACCCAGGCTTGTCTGTGACAGTGGAGGTTCCAGGTCGGCCCTGCGCTCGGC 540
Db 293 CTCTGCTGACCCAGGCTTGTCTGTGACAGTGGAGTTCAGGTCGGTCTCTGCGCTCGGC 234
Qy 541 GTCTCGCGCGCGCA-CAGCTTGGGTGGCTCGCTACATTTTGAGGAAAACGCTAGACCT 599
Db 233 GTCTCGCGCGCGCAAGCTCTGGGTGCTCGCTACATTTTGAGGTAGACGCTAGATCA 174
Qy 600 GCCCCTCGCGCGCTGTGTCTCGTCTTCTTCCTCCG--CCGAGACATGGCGTGTCTTGGCAAC 657
Db 173 CTAGACCTGTCTCGCGCATCGCGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 114
Qy 658 TTGCGGTGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 714
Db 113 ATGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 54
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genomic survey sequence.
CC937355
CC937355.1 GI:33623181
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 681)
Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
and Wing,R.
REFERENCE
AUTHORS TITLE
Sequencing of the maize genome
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
```

Tel: 520 626 3967		Fax: 520 621 9288		Email: http://genome.arizona.edu	
PCR Primers		PCF Primers		FORWARD: T7	
BACKWARD: ML3r		Plate: 0227 row: P column: 18		Seq primer: ML3r	
Class: BAC ends.		Location/Qualifiers		1. 681	
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		Best Local Similarity		91.8%; Pred. No. 1.1e-112;	
		Matches 640; Conservative		0; Mismatches 36; Indels 21; Gaps 6;	
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Db	2	GTTCCTCGGNGACACACACACACACCGCGGAGCCACATATACGTGTAGCTCGCCCGGTC	61		
Qy	960	GGAACTCGGCAAGTGTCAAAGCAAGCTTTCAACGGATGCCATGCTTCGCGCGCGCGG	1019		
Db	62	GSACTCGGCAAGT-----AGGCAAGCTTTCAACGGATGCCATGCTTCGCGCGCGCGG	116		
Qy	1020	GAGAGCTTGGCGGAGGACCTGCTCATCGCGATCGGATACGAGCGTTGGATCGGAGATC	1079		
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Qy	1080	GGAGCGCTTTTGGACITTTTGGCCCTGTCTATCTCATCTGCTACCGTGTACCGTGTGGCGTGTCTCC	1139		
Db	177	GGAGCGCTTTTGGACITTTTGGCCCTGTCTATCTCATCTGCTACCGTGTGGCGTGTCTCC	236		
Qy	1140	ATGATATATATATGTTTGTAAATTTGCAAAATCTGTATGTAAATAAAATAAAATAAAAT	1199		
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Qy	1200	GAAGTAGTATCAGAACTCATCGAGCTCGAAATAACCGTAGAATGACCGGACGTCGGCA	1259		
Db	292	CAGTAGTATCAGAACTCATCGAGCTCGAAATAACCGTAGAATGACCGGACGTCGGCA	351		
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Db	352	G-----GTGCAGTTGAAGCTTGAATAACCGTTAGGCTTGGCCCTCGTTATTAGAGAGCTC	406		
Qy	1320	ACGTAACATATCTCTCTATCTCTACTACTATTGATTAATAATTTCTACTACTATTAAATAA	1379		
Db	407	ACGTAACATATCTCTCTATCTCTACTACTATTGATTAATAATTTCTACTACTATTAAATAA	466		
Qy	1380	ATATACAAGTTTCTCCCTTCATACATGGTTTCCCTCTCCAAAGCGCGCTTTTCCACTTGTG	1439		
Db	467	ATATACAGTTTCCGCCCTTCAAGTGGTTTCTCTCCAGCGCGCTTTTCCACTTGTG	526		
Qy	1440	AAAAATGACAACTGACACACTTGTCTATTTATCTATATATAAGGATTAATACTACAAAAA	1499		
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Qy	1500	ATATACAATACATCCATTCGGATTTTATAATTCGTATCA-ATTTTTTCCACCAAGTTTCATC	1558		
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 QY 541 GTCTCGGCGCGGGA-CAGCTTGGGTGGGCTCGCTACATCTTTGAGGAAACCGTAGAC-- 597
 Db 123 GTCTCGGCGCGGACAGCTCTGGGTGGTCTGCTACATCTTTGAGTAGACGCTAGACCA 64
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RESULT 9
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 DEFINITION OGKMW20TV ZM 0.7-1.5 kb Zea mays genomic clone ZMMBMA0664D15,
 genomic survey sequence.

ACCESSION CG2211794
 VERSION CG2211794.1 GI:34121682
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 802)
 AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

TITLE Consortium for Maize Genomics
 JOURNAL Unpublished (2002)
 COMMENT Other GSSs: OGKMW20TH
 Contact: Cathy Whitelaw
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TF
 Class: sheared ends.

FEATURES
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 methylation filtered genomic DNA library"

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 Best Local Similarity 86.9%; Pred. No. 2.3e-104;
 Matches 602; Conservative 0; Mismatches 52; Indels 39; Gaps 3;
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 145 CCATGGTCGGTACCTTCCCTGCGTGCAGAAATGAACCGACCTGTTGCGTACAGACATT 204
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 265 AGTACACCTTCTCCAGAGGACCAAGTGGCTCTCGGTTGGCGCTGGCGGCTACC 324

QY 181 CTGCGCCTCAGTAGATTAGATGATCTGCGTGCCTCCAGGCTCCAGCCATATCGATGCG 240
 Db 325 CTGCGCCTCAGTAGATTAGATGATCTGCGTGCCTCCAGGCTCCAGCCATATCGATGCG 384
 QY 241 TTTGATCAGCTGACGGAATGATCTCTGCGAGGGAATTTACTACTGCGCGCTCGAGCGGAC 300
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 Db 505 GACATCAGTGGCATCAACGCGGAGGTATGTCGCGGAGGTACAGCGTGTCTAGCT 556
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RESULT 10
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 DEFINITION ZMMBB0371K12.r ZMMBBB Zea mays genomic clone ZMMBBB0371K12 3',
 genomic survey sequence.

ACCESSION CG891370
 VERSION CG891370.1 GI:38645788
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 627)
 AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
 and Wing,R.

TITLE Sequencing of the maize genome
 JOURNAL Unpublished (2003)
 COMMENT Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 488A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: T7
 BACKWARD: M13r
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FEATURES
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  genomic survey sequence.
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VERSION
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    clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 737)
  Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
  Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  Consortium for Maize Genomics
  Unpublished (2002)
  Other GSSs: OGBABN93T
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
  Seq primer: TF
  Class: sheared ends.
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  Query Match 11.3%; Score 288.6; DB 8; Length 737;
  Best Local Similarity 79.5%; Pred. No. 2.5e-55;
  Matches 459; Conservative 0; Mismatches 69; Indels 49; Gaps 8;
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  Qy 360 CGACATCAGTGGCATCAACGGGAGGTCATGCCGGGCGGACAGGTACAGCGTGTCTTAGC 419
  Db 677 CGACATCAGTGGCATCAACGGGAGGTCATGCCGGGCGGACAGGTACAGCGTGTCTG 625
  Qy 420 TACCTTGTCTTTAACTGCACACTGCACCTCTGCACACTGCACAGCTAGTATGCTGCTA 479
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  Qy 480 TCTCTGTGTACCCAGGCTTCTTGTGGACAGTGGAGTTCACAGTCCGCGCTGCGGTCGG 539
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  Db 472 ACTAGACCTGCTGCTCGCATCGCGCTGTGTCAGTTCCTTCTTCTTCCGCCAGA 413
  Qy 657 CTTTGGCGTGTGAGTGTGTTTGTCTGATGAGAGC--TGTCCTTTTCCCTGTGATGCGAG 713
  Db 412 CATGGCGTGTGAGTGTGTTTGTCTGATGAGAGCTTTCTTCTTCCCTGTGATGCGAG 353
  Qy 714 AGGAT-ACCAGATCGCGCGGCTGTGCTTCTTCCAGCCCAA--CCAATTCGCTAGC 770
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  Qy 771 A-TTCGCTACCAACATTTTGGGTTTGTATATGTTGGTCTCTCTATCTCTGTGCTCAT 829
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    genomic survey sequence.
  ACCESSION
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  VERSION
    CG865571.1 GI:38506429
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  SOURCE
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    Zea mays
    ORGANISM
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      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
      clade; Panicoideae; Andropogoneae; Zea.
      1 (bases 1 to 344)
      Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
      and Wing,R.
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TITLE	JOURNAL	COMMENT
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Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0339 row: 0 column: 17
Seq primer: T7
Class: BAC ends.

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. Robustness: The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. Interpretability: The model's predictions are interpretable, allowing users to understand the underlying factors influencing the outcome.	Model Performance Metrics
4. Scalability: The model is scalable, capable of handling large volumes of data and complex tasks efficiently.	Model Performance Metrics
5. Real-time Processing: The model is designed for real-time processing, enabling immediate decision-making based on incoming data.	Model Performance Metrics
6. Integration with Existing Systems: The model seamlessly integrates with existing systems, facilitating a smooth transition and adoption.	Model Performance Metrics
7. Customizable Parameters: The model offers customizable parameters, allowing users to tailor the model to specific requirements.	Model Performance Metrics
8. Comprehensive Documentation: The model is accompanied by comprehensive documentation, providing detailed information on its usage and capabilities.	Model Performance Metrics
9. Regular Updates: The model is regularly updated with the latest data and insights, ensuring its relevance and accuracy over time.	Model Performance Metrics
10. Support and Maintenance: The model is supported by a dedicated team, ensuring timely assistance and maintenance for any issues.	Model Performance Metrics

ORIGIN

Query Match	11.1%;	Score 283.4;	DB 9;	Length 344;
Best Local Similarity	91.7%;	Pred. No. 3.6e-54;		
Matches 311;	Conservative 0;	Mismatches 23;	Indels 5;	Gaps 1;
QY	1161	AATTGCCAAATTCGTATGTAAATAAAATAAAATCAAATCAAGTAGTATCAGAAATGATCG	1220	
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	1	AANNGCCAAACTATTTTGTAAATAAAATAAAATAAAATCAAGTAGTATCAGAAATGATCG	60	
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	61	GAGCTCGAAAATACCGTAAGAAGACCGGACGCTGCGGCGAG-----GTGCGAGTTGAAGCTT	115	
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	79.2	3.1	1068	US-09-786-534-1	Sequence 1, Appli
2	79.2	3.1	1534	US-09-786-534-3	Sequence 3, Appli
3	74.4	2.9	2075	US-09-270-767-10495	Sequence 10495, A
C 4	68	2.7	601	US-09-949-016-70542	Sequence 70542, A
C 5	68	2.7	601	US-09-949-016-70543	Sequence 70543, A
6	68	2.7	2226	US-09-799-451-355	Sequence 355, App
7	68	2.7	2727	US-09-814-915A-36	Sequence 36, Appl
8	68	2.7	2813	US-09-949-016-2085	Sequence 2085, Ap
9	68	2.7	12981	US-09-949-016-13827	Sequence 13827, A
10	66.6	2.6	187169	US-09-949-016-12776	Sequence 12776, A
11	66.6	2.6	191569	US-09-949-016-15940	Sequence 15940, A
12	66.4	2.6	13254	US-08-276-852-156	Sequence 156, App
C 13	66.4	2.6	13254	US-08-276-852-170	Sequence 170, App
C 14	66.4	2.6	13254	US-08-899-575-156	Sequence 156, App
C 15	66.4	2.6	13254	US-08-899-575-170	Sequence 170, App
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18	66.4	2.6	13254	PCT-US95-08743-156	Sequence 156, App
C 19	66.4	2.6	13254	PCT-US95-08743-170	Sequence 170, App
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C 21	66.4	2.6	105919	US-09-949-016-11769	Sequence 11769, A
C 22	65.2	2.6	601	US-09-949-016-30531	Sequence 30531, A
C 23	65.2	2.6	601	US-09-949-016-30532	Sequence 30532, A
C 24	65.2	2.6	601	US-09-949-016-37150	Sequence 37150, A
C 25	65.2	2.6	601	US-09-949-016-37151	Sequence 37151, A
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C 29	65.2	2.6	601	4	US-09-949-016-145869	Sequence 145869,
C 30	65.2	2.6	601	4	US-09-949-016-146136	Sequence 146136,
C 31	65.2	2.6	601	4	US-09-949-016-146137	Sequence 146137,
C 32	65.2	2.6	601	4	US-09-949-016-146404	Sequence 146404,
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38	65.2	2.6	223471	4	US-09-949-016-12724	Sequence 12724, A
39	65.2	2.6	223471	4	US-09-949-016-12725	Sequence 12725, A
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C 45	63.2	2.5	601	4	US-09-949-016-168056	Sequence 168056,

ALIGNMENTS

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US-09-786-534-1
; Sequence 1, Application US/09786534
; Patent No. 6727095
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; APPLICANT: Tischner, Rudolf
; APPLICANT: Hoffmann, Guido
; TITLE OF INVENTION: GENETICALLY MODIFIED SUGARBET
; FILE REFERENCE: P/2107-170
; CURRENT APPLICATION NUMBER: US/09786.534
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/EP99/06522
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 198 40 964.8
; PRIOR FILING DATE: 1998-09-08
; NUMBER OF SEQ ID NOS: 3
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; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Beta vulgaris
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; NAME/KEY: CDS
; LOCATION: (1)..(1068)
US-09-786-534-1

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; Patent No. 6727095
; GENERAL INFORMATION:
; APPLICANT: Tischner, Rudolf
; APPLICANT: Hoffmann, Guido

Qy 391 CCGGGCAGGTA 402
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Db 354 CCGCCAGGTA 343

RESULT 6

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; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 355
; LENGTH: 2226
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (211)..(1212)
US-09-799-451-355

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Best Local Similarity 69.7%; Pred. No. 1.2e-07;
Matches 92; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTGCGCGCTCGGAGCGGACAGTCTTACGGCGGGGACATCGTGGAC 327
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Db 598 CAGGTCCATATTACTGTGGTGGAGACAGACAGGCTATGGCAGGACATCGTGGAG 657
Qy 328 GCGCACTACAAGCGCTCTTACCGCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db 658 GCCATTACCGGCGCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTC 717
Qy 388 ATGCCGGGCGAG 399
Db 718 ATGCTGCCCGAG 729

RESULT 7

US-09-814-915A-36
; Sequence 36, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
; TITLE OF INVENTION: Thereto
; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A

; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 2727
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-36

Query Match 2.7%; Score 68; DB 4; Length 2727;
Best Local Similarity 69.7%; Pred. No. 1.3e-07;
Matches 92; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTGCGCGCTCGGAGCGGACAGTCTTACGGCGGGGACATCGTGGAC 327
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Db 581 CAGGTCCATATTACTGTGGTGGAGACAGACAGGCTATGGCAGGACATCGTGGAG 640
Qy 328 GCGCACTACAAGCGCTCTTACCGCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db 641 GCCATTACCGGCGCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTC 700
Qy 388 ATGCCGGGCGAG 399
Db 701 ATGCTGCCCGAG 712

RESULT 8

US-09-949-016-2085
; Sequence 2085, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2085
; LENGTH: 2813
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2085

Query Match 2.7%; Score 68; DB 4; Length 2813;
Best Local Similarity 69.7%; Pred. No. 1.4e-07;
Matches 92; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTGCGCGCTCGGAGCGGACAGTCTTACGGCGGGGACATCGTGGAC 327
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Db 558 CAGGTCCATATTACTGTGGTGGAGACAGACAGGCTATGGCAGGACATCGTGGAG 617
Qy 328 GCGCACTACAAGCGCTCTTACCGCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db 618 GCCATTACCGGCGCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTC 677
Qy 388 ATGCCGGGCGAG 399
Db 678 ATGCTGCCCGAG 689

RESULT 9

US-09-949-016-13827
; Sequence 13827, Application US/09949016

Qy 1705 AAAAGTCAATGATTAGATTAAATTCATGACATATGCTAATAATTTTAAATA 1764
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Db 1023 TAAATATATATATAAATATATATATATATATATATATATATATATATATA 1082
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Qy 1765 TAAAAA 1771
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Db 1083 TATAATA 1089
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RESULT 12

US-08-276-852-156
; Sequence 156, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-276-852-156

Query Match 2.6%; Score 66.4; DB 1; Length 13254;
Best Local Similarity 68.9%; Pred. No. 9.3e-07;
Matches 91; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Qy 268 CAGGACCTTACTACTGCGCGTCGAGCGGACAAAGTCCTTACGGCGGGACATCGTGGAC 327
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Db 8839 CAAGTCCGTATTACTGTGGTGTGGCGCAGACAAAGCCTATGGCAGGGATATCGTGGAG 8898
|||||
Qy 328 GCGCACTACAAGGCTCTCTACCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
|||||
Db 8899 GCTCACTACCGCGCTCTGTATGCTGGGGTCAAGATTACAGGAACAAATGCTGAGGTC 8958
|||||
Qy 388 ATGCCGGGGCAG 399
|||||

Db 8959 ATGCTGCCAG 8970
|||||

RESULT 13

US-08-276-852-170/c
; Sequence 170, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-276-852-170

Query Match 2.6%; Score 66.4; DB 1; Length 13254;
Best Local Similarity 68.9%; Pred. No. 9.3e-07;
Matches 91; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Qy 268 CAGGACCTTACTACTGCGCGTCGAGCGGACAAAGTCCTTACGGCGGGACATCGTGGAC 327
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Db 4416 CAAGTCCGTATTACTGTGGTGTGGCGCAGACAAAGCCTATGGCAGGGATATCGTGGAG 4357
|||||
Qy 328 GCGCACTACAAGGCTCTCTACCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
|||||
Db 4356 GCTCACTACCGCGCTCTGTATGCTGGGGTCAAGATTACAGGAACAAATGCTGAGGTC 4297
|||||
Qy 388 ATGCCGGGGCAG 399
|||||
Db 4296 ATGCTGCCAG 4285
|||||

RESULT 14

US-08-899-575-156
; Sequence 156, Application US/08899575
; Patent No. 5770440

GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-899-575-156

Query Match 2.6%; Score 66.4; DB 1; Length 13254;
Best Local Similarity 68.9%; Pred. No. 9.3e-07;
Matches 91; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTCGCGCGTGGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 327
Db 8839 CAAGGTCGGTATTACTGTGTGGCGCAGACAAAGCCTATGGCAGGGATATCGTGGAG 8898

Qy 328 GCGCACTACAGGCGCTCTTACGGCGGCATCGACATCAGTGGCATCAACGGGGAGTGC 387
Db 8899 GCTCACTACCGCGCTCTTGTATGCTGGGGTCAAGATTACAGGAACAAATGCTGAGGTC 8958

Qy 388 ATGCCGGGGCAG 399
Db 8959 ATGCCTGCCAG 8970

RESULT 15
US-08-899-575-170/c
; Sequence 170, Application US/08899575
; Patent No. 5770440

GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-899-575-170

Query Match 2.6%; Score 66.4; DB 1; Length 13254;
Best Local Similarity 68.9%; Pred. No. 9.3e-07;
Matches 91; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTCGCGCGTGGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 327
Db 4416 CAAGTCCGTATTACTGTGTGGCGCAGACAAAGCCTATGGCAGGGATATCGTGGAG 4357

Qy 328 GCGCACTACAGGCGCTCTTACGGCGGCATCGACATCAGTGGCATCAACGGGGAGTGC 387
Db 4356 GCTCACTACCGCGCTCTTGTATGCTGGGGTCAAGATTACAGGAACAAATGCTGAGGTC 4297

Qy 388 ATGCCGGGGCAG 399
Db 4296 ATGCCTGCCAG 4285

Search completed: April 27, 2005, 20:23:43
Job time : 419 secs